# Prevalence of *BRCA1* and *BRCA2* pathogenic variants in a large, unselected breast cancer cohort

Original research


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**WORD COUNT**

3,661

**KEYWORDS**

*BRCA1*; *BRCA2*; clinical testing; next-generation sequencing; screening criteria; prediction; breast cancer

**RUNNING TITLE**

*BRCA* testing for all newly-diagnosed breast cancer patients?

**DISCLOSURE OF POTENTIAL CONFLICT OF INTEREST**

Helene Nordahl Christensen and Astrid Torstensson are employed by AstraZeneca. No other author declared competing financial interests.

**ABSTRACT**

Breast cancer patients with *BRCA1/2*-driven tumors may benefit from targeted therapy. It is not clear whether current *BRCA* screening guidelines are effective at identifying these patients. The purpose of this study was to evaluate the prevalence of inherited *BRCA1/2* pathogenic variants in a large, clinically representative breast cancer cohort and to estimate the proportion of *BRCA1/2* carriers not detected by selectively screening individuals with the highest probability of being carriers according to current clinical guidelines. The study included 5,122 unselected Swedish breast cancer patients diagnosed from 2001 to 2008. Target sequence enrichment (48.48 Fluidigm Access Arrays) and sequencing were performed (Illumina Hi-Seq 2500 instrument, v4 chemistry). Differences in patient and tumor characteristics of *BRCA1/2* carriers who were already identified as part of clinical *BRCA1/2* testing routines and additional *BRCA1/2* carriers found by sequencing the entire study population were compared using logistic regression models. Ninety-two of 5,099 patients with valid variant calls were identified as *BRCA1/2* carriers by screening all study participants (1.8%). Only 416 study participants (8.2%) were screened as part of clinical practice, but this identified 35 out of 92 carriers (38.0%). Clinically-identified carriers were younger, less likely postmenopausal and more likely to be associated with familiar ovarian cancer compared to the additional carriers identified by screening all patients. More *BRCA2* (34/42, 81.0%) than *BRCA1* carriers (23/50, 46%) were missed by clinical screening. In conclusion, *BRCA1/2* mutation prevalence in unselected breast cancer patients was 1.8%. Six in ten *BRCA* carriers were not detected by selective clinical screening of individuals.

**NOVELTY AND IMPACT**

This is one of the largest studies on *BRCA1/2* prevalence in an unselected breast cancer population.

## INTRODUCTION

Estimates of the prevalence of *BRCA1* or *BRCA2* germline pathogenic variants vary considerably depending on the technology used for mutation screening, population size, and to what extent the genes are tested [1]. Although *BRCA1/2* pathogenic variants are major determinants of hereditary breast cancers, women diagnosed with *BRCA1/2*-associated breast cancer do not necessarily exhibit worse survival patterns than breast cancer patients without such pathogenic variants [2]. On the contrary, patients diagnosed with *BRCA1/2*-associated breast cancers have advantages in terms of treatment options when compared to patients with *BRCA1/2* wild-type breast cancer (reviewed in [3]). Evidence from clinical trials showed significantly greater sensitivity and higher response rate of *BRCA1/2*-associated cancers to neoadjuvant and standard adjuvant chemotherapy than their wild-type *BRCA1/2* counterparts [3]. Treatment options for *BRCA1/2* breast cancers are also broadened with the introduction of new therapeutic agents, such as poly (ADP-ribose) polymerase (*PARP*) inhibitors, which selectively target *BRCA1/2*-deficient cancer cells [4-7].

Recommendation for counselling and genetic screening for *BRCA1/2* pathogenic variants is mainly based on personal and family history of breast and/or ovarian cancer, young age at disease onset, male breast cancer and multiple tumors (bilateral breast cancer or breast and ovarian cancer in the same patient) [8]. However, *BRCA* testing guidelines vary by region and country [9, 10]. In Sweden, the Swedish Breast Cancer Group *BRCA1* and *BRCA2* screening criteria are used [8]. A report by Nilsson *et al*. estimated that the Swedish *BRCA* testing criteria has an effectiveness of only 18% and concluded that clinical genetic testing criteria for *BRCA1* and *BRCA2* should be critically revised [8]. As the effective identification of *BRCA1*/*2* germline pathogenic variants has potential to influence treatment decision and has implications for the family of the patients [3-6, 11, 12], the pros and cons of testing all women diagnosed with breast cancer for such pathogenic variants need to be examined. In a large, clinically representative breast cancer cohort, we examined the prevalence and characteristics of *BRCA1/2* germline mutation carriers and compared our results with *BRCA* mutation carriers already identified through a national clinical *BRCA* screening program.

## METHODS

### Study participants

All women under the age of 80 and diagnosed with breast cancer from 2001 to 2008 in Stockholm, Sweden were identified through the Stockholm-Gotland Regional Breast Cancer quality register [13, 14]. Women were invited to participate in the LIBRO1 study in 2009. In all, 5,715 women of the LIBRO1 study gave informed consent to the retrieval of data from medical records and national registers, answered a detailed questionnaire on background and lifestyle risk factors, and provided a blood specimen for genetic analysis [13, 14]. Of these women, 5,125 were successfully genotyped in a large-scale genotyping study on breast cancer risk (see **eTable 1** in **Data Supplement 1** for exclusion criteria, online only) [15]. Of these women, 5,122 had enough DNA remaining for targeted sequencing. The final analytical dataset comprised 5,099 samples which passed quality control. This study was approved by the Regional Ethical Review Board in Stockholm, Sweden (Karolinska Institutet, DNR2009/254-31/4).

### Patient characteristics

Self-reported information on education level, age at menarche, body mass index (BMI), number of children, oral contraceptive use, hormone replacement therapy, and details of family history of breast and ovarian cancer were obtained from the questionnaire. Patients were asked if their biological mothers and sisters have been diagnosed with breast or ovarian cancer, and if so, at what age. Mammograms were retrieved from radiology departments. Percent mammographic density was measured using an automated method described in [16]. Information on whether the patients have an ovarian cancer or any non-breast malignancy was retrieved via linkage to the Swedish Cancer Register using unique personal identity numbers of study participants (*personnummer*, ten or twelve digit number used in Sweden to identify individuals) [17].

### Tumor characteristics

Tumor characteristics were retrieved from the Stockholm-Gotland Regional Breast Cancer Quality Register [18, 19] using unique personal identity numbers [17]. Tumor size was measured in millimetres. Lymph node involvement was dichotomized into positive or negative. Estrogen receptor (ER) status was recorded as negative or positive in the registers, determined by radioimmunoassay or

immunohistochemistry with cutoff values of more than 10% positive cells for IHC and more than 0 fmol/µg DNA for radioimmunoassay assays. The completeness of the registry data was 98% for tumor size and lymph node status and 80% for ER status. Information on grade (Nottingham histologic grade for invasive cancer and nuclear grade for cancer *in situ*) was available from 2004, with 93% completeness [19].

Data on molecular markers were retrieved in 2015–2016 from medical and pathology records at treating hospitals (previously described in [20]). HER2 status was dichotomized (positive/negative) in accordance with the Swedish Society of Pathology's guidelines: negative if protein expression showed 0 or 1+, or was higher with no confirmed gene amplification by FISH, and positive if FISH showed gene amplification.[20] Proliferation marker Ki67 was measured according to contemporary guidelines and reported as percent staining (low if <20% and high otherwise).[20] HER2 and Ki67 markers were not assessed, and thus not available in medical records, prior to 2005. Breast cancer subtype was assigned using a random forest algorithm (caret R package, v. 6.0.58) described in [20]. The algorithm was trained to predict subtype based on a subset of individuals with PAM50 subtype derived from gene expression data (*n*=237). Breast cancer subtype was then assigned to the remaining cases based on age at diagnosis, ER, PR, HER2, and Ki67 status.

**Targeted sequencing and data processing**

Target-enriched sequencing libraries of germline DNA from 5,122 breast cancer patients were prepared at the Centre for Cancer Genetic Epidemiology (University of Cambridge), as part of a larger effort that included samples from other cohorts. Briefly, target sequence enrichment was performed using 48.48 Fluidigm Access Arrays according to the manufacturer's protocol (Fluidigm, South San Francisco, California, USA). Fluidigm D3 assay design software was used to select primer pairs, which were multiplexed into pools selected for GC content and avoidance of off-target primer-primer and primer-product complementarity (**eTable 2** in **Data Supplement 2**). Target sequences were amplified with Illumina sequencing adaptors and one of 1,536 unique sample barcodes (supplied by Fluidigm, South San Francisco, California, USA). Robotic liquid handling and barcode plate identification were used in all steps of the library preparation process. The amplicon library was quantified with the KAPA Library Quantification Kit (KapaBiosystems, Boston, Massachusetts, USA) and then sequenced on the Illumina Hi-Seq 2500 instrument using v4 chemistry, according to the

manufacturer's protocol (Illumina, San Diego, California, USA). Each library was sequenced 2-3 times to provide sufficient coverage. Details on sequence data processing and quality control are shown in **eMethods** in **Data Supplement 1**. A total of 5,099 samples had valid variant calls. The mean read depth across the coding sequences of *BRCA1* and *BRCA2* was 792.2 (standard deviation: 587.4) and 631 (standard deviation: 516), respectively. More than 90% of targeted bases had more than 15x coverage (94.8 [15.9] and 92.5 [20.4] for *BRCA1* and *BRCA2*, respectively).

**Definition of pathogenic variants**

As described previously in Borg *et al*. [21], sequence variants were categorized based on their predicted effect on the mRNA and amino acid level and defined as pathogenic if they were (1) frameshift and nonsense variants with the exception of the *BRCA2* c.9976A>T (BIC: K3326X) and other variants located 3' thereof (*n*=105), and (2) all consensus splice acceptor or donor sequence sites, except those predicted to lead to naturally occurring in-frame RNA isoforms that may rescue gene function [22]. Public data on pathogenic *BRCA* variants (includes frameshift insertion/deletions, nonsense, splice sites and missense variants conclusively demonstrated to be pathogenic) that have been curated and classified by an international expert panel, the ENIGMA consortium, were also downloaded from http://brcaexchange.org/ (access date: Feb 22, 2017) for the annotation of the sequence data.

**Identification of women who have undergone *BRCA* testing in Sweden**

Mutation screening for all oncogenetic clinics in Sweden (Lund, Stockholm, Uppsala, Göteborg, Linköping and Umeå) were conducted at the Department of Oncology, Lund University as part of a national *BRCA* testing program (**eMethods** in **Data Supplement 1**). We cross-referenced the personal identity numbers of all study participants in LIBRO1 with the *BRCA* testing unit at Lund University to identify women who have been tested for *BRCA1/2* pathogenic variants previously. The SweBRCA criteria are the only *BRCA1/2* testing criteria used in Sweden (**eTable 3** in **Data Supplement 1**) [8]. Clinicians do not have any obligation to comply with the guidelines [8].

**Statistical analysis**

Predictor variables which include patient and tumor characteristics were described by the counts of each category and corresponding proportions. Binary logistic regression models were fitted

for the dichotomous outcome (*BRCA1* [reference] and *BRCA2*), and multinomial logistic regression models were fitted for the three-category outcome (*BRCA1*, *BRCA2* and non-*BRCA* [reference category]), adjusting for age and year of diagnosis. Logistic regression models were also used to compare estimates (odds ratios [OR] and corresponding 95% confidence intervals [CI]) of patient and tumor characteristics between *BRCA1/2* carriers already identified among a subset of 416 patients screened as part of clinical *BRCA* testing routines and additional *BRCA1/2* carriers found by sequencing the entire study population (i.e. those not tested by the Swedish *BRCA* testing program).

## RESULTS

The median time from date of diagnosis to study entry is 4.8 years (range: 1.3 to 9.2). The median age of breast cancer diagnosis of the study cohort was 59.6 years (range: 25.1 to 79.9). Nine of ten breast cancers were invasive (89.4%).

### Spectrum of *BRCA1* and *BRCA2* pathogenic variants

Of the 5,099 breast cancer patients, 92 (1.8%) were identified as *BRCA1/2* carriers (50 *BRCA1* carriers and 42 *BRCA2* carriers) and 5,007 were non-*BRCA*.

Among the 50 *BRCA1* carriers, there were 28 unique germline *BRCA1* pathogenic variants (11 frameshift deletions, 2 frameshift insertions, 8 truncating, 4 splice sites, and 3 missense) (**Figure 1** and **eTable 4** in **Data Supplement 1**). Frameshift insertions and deletions made up 26/50 (52%) of the *BRCA1* pathogenic variants. Exon 11 harbored 33/50 (66%) of the *BRCA1* pathogenic variants. The most common pathogenic variant was c.3048_3052dupTGAGA (*n*=8), which is a founder mutation originating from the West coast of Sweden [23]. Three other Swedish founder pathogenic variants were also identified (c.1082_1092del [*n*=5], c.2475delC [*n*=2]) and c.3626delT [*n*=3]) [23-26].

Among the 42 *BRCA2* carriers, there were 33 unique *BRCA2* pathogenic variants (18 frameshift deletions, 3 frameshift insertions, 9 truncating, and 3 splice sites) (**Figure 2** and **eTable 5** in **Data Supplement 1,** only online). Over half of all *BRCA2* carriers (24/42, 57.1%) had a pathogenic variant on exon 11.

### Patient characteristics of *non-BRCA*, *BRCA1* and *BRCA2* carriers

Half of the non-*BRCA* women were at least 60 years old, compared to 26.0% and 33.3% for women with *BRCA1* and *BRCA2* pathogenic variants, respectively (**eTable 6** in **Data Supplement 1**).

In the crude analyses controlling for age and year of diagnosis, *BRCA1* and *BRCA2* carriers were more likely than non-*BRCA* women to report family history of both breast ($OR_{BRCA1 \text{ vs non-}BRCA}$: 4.00 [2.27 to 7.05] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 2.23 [1.17 to 4.26]) and family history of ovarian cancer ($OR_{BRCA1 \text{ vs non-}BRCA}$: 7.53 [3.82 to 14.82] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 3.62 [1.50 to 8.71]) (**eTable 6** in **Data Supplement 1**). *BRCA1* carriers, in particular, were also more likely to be also diagnosed with an ovarian cancer themselves ($OR_{BRCA1 \text{ vs non-}BRCA}$: 28.02 [10.72 to 73.29] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 8.11 [1.87 to 35.24]) than non-*BRCA* patients (**eTable 6** in **Data Supplement 1**). *BRCA1* carriers were more likely to have a personal history of another malignant cancer in addition to their breast cancer than patients with non-*BRCA* patients ($OR_{BRCA1 \text{ vs non-}BRCA}$: 2.93 [1.37 to 6.27]). This association was driven by ovarian cancers ($OR_{BRCA1 \text{ vs non-}BRCA}$ for all non-breast and non-ovarian malignancies: 0.83 [0.25 to 2.73]). *BRCA2* carriers were significantly less likely to be ever users of hormone replacement therapy (HRT) than non-*BRCA* breast cancer patients (26.2% vs 53.8%) (**eTable 6** in **Data Supplement 1**). In multivariable models shown in **Table 1**, all variables remained significantly associated, with the exception of personal history of any non-breast malignancy.

**Tumor characteristics of *non-BRCA*, *BRCA1* and *BRCA2* carriers**

In the crude analyses controlling for age and year of diagnosis, *BRCA2* carriers were in general not significantly different from non-*BRCA* women in terms of tumor characteristics, with the exception of nodal involvement ($OR_{BRCA2 \text{ vs non-}BRCA}$: 2.71 [1.31 to 5.62], **eTable 7** in **Data Supplement 1**). On the contrary, tumors of *BRCA1* carriers were more aggressive than those of non-*BRCA* breast cancer patients for all tumor characteristics examined (ER and PR status, grade, tumor size, nodal involvement, and breast cancer subtype) except for the proportion of invasive tumors (**eTable 7** in **Data Supplement 1**).

In multivariable multinomial models including all tumor characteristics that were significantly different between non-*BRCA* and *BRCA1*-positive breast cancer patients, only ER-negativity remained significant ($OR_{BRCA1 \text{ vs non-}BRCA}$: 5.19 [2.68 to 10.06]) (**Table 1**). ER status was also the only independent tumor characteristic that distinguished between *BRCA1* and *BRCA2* carriers ($OR_{BRCA2 \text{ vs } BRCA1}$: 0.22 [0.07 to 0.77]). This observation was mirrored in a separate multinomial model considering breast cancer subtypes, where *BRCA1* tumors were found to be 40 times more likely to be of the basal-like subtype ($OR_{BRCA1 \text{ vs non-}BRCA}$: 40.07 [14.26 to 112.59]). Only nodal involvement remained

significant in the comparison between *BRCA2* and non-*BRCA* breast cancer cases in the multivariable model ($OR_{BRCA2 \text{ vs non-}BRCA}$: 2.54 [1.20 to 5.37) (**Table 1**).

**Comparison of *BRCA1/2* carriers identified versus not identified through clinical screening**

Linkage with the Swedish *BRCA* register found 416 patients (8.2%) that were screened for pathogenic variants as part of routine clinical practice. Among these 416 women, clinical screening identified 39 carriers in the study cohort, of which our study confirmed 35 (**Figure 3**). Four pathogenic variants were missed (*BRCA1*: c.4186-1785_4358-1667dup and c.4358-1729_4986+736dup; *BRCA2*: c.7805+1538_8331+560del and c.9097_9098insT) (**Figure 3**). Three of these were large exonic deletions or duplications that the Fluidigm Access Array system is not suitable for detecting. This gives the Fluidigm Access Array method an estimated sensitivity of about 90%, or 97% when excluding large exonic variants.

Overall, 57/92 carriers (62.0%) were not already clinically identified: Two additional carriers were detected by the Fluidigm Access Array method among clinically screened patients (*BRCA2*: c.2578delA [confirmed by Sanger sequencing to be a false positive] and c.7443delT [missed carrier, screened with DHPLC and MLPA in 2008]); the remaining 55 out of 92 carriers (59.8%) identified by the Fluidigm Access Array method in the complete study cohort were never screened as part of clinical routine (**Figure 3**).

More *BRCA2* (34/42, 80%) than *BRCA1* pathogenic variants (23/50, 46%) were missed by selectively testing only high-risk individuals who were recommended for genetic testing and counselling (**Table 2**). Controlling for only year of diagnosis, *BRCA* carriers identified by clinical routine screening were younger (37.2% aged 50 years and above, compared to 73.7%), less likely to have experienced menopause ($OR_{\text{identified versus not identified}}$: 0.17 [0.07 to 0.44]) and more likely to be associated with a family history of ovarian cancer ($OR_{\text{identified versus not identified}}$: 3.11 [1.06 to 9.09]) (**Table 2**). Further adjustment for gene revealed a significant association with age at menarche ($OR_{\text{identified versus not identified}}$: 2.99 [1.00 to 8.94]). There was also a trend between the likelihood of being identified as a carrier by selective testing and more children (**Table 2**). Tumors of *BRCA1/2* carriers identified by selective testing were more often detected clinically ($OR_{\text{identified versus not identified}}$: 5.52 [1.38 to 22.18]), higher grade ($OR_{\text{identified versus not identified}}$: 0.28 [0.08 to 0.92]), larger size ($OR_{\text{identified versus not identified}}$: 2.48 [1.00 to 6.16]) and of a basal subtype ($OR_{\text{identified versus not identified}}$: 6.07 [1.49 to 24.76]) (**eTable 8** in **Data**

**Supplement 1**). The differences observed for all tumor characteristics and selective testing detection did not remain significant after adjusting for gene.

## DISCUSSION

*BRCA1/2* pathogenic variants were found in 1.8% of unselected breast cancer patients. In contrast to studies reporting *BRCA1/2* prevalence for a subset of high risk women [27, 28], the present sample reflects the general breast cancer population. None of the breast cancer risk factors examined differed between *BRCA1* and *BRCA2* carriers. However, *BRCA1* and *BRCA2* breast cancers differed in the proportions of patients with ER-negative disease and basal-like subtype. Six out of ten *BRCA1/2* carriers were not identified through genetic testing in the clinic.

*BRCA1* and *BRCA2* mutation frequencies in breast and ovarian cancer patients unselected for family history or age at onset are generally low (<1–7% for *BRCA1* and 1–3% for *BRCA2*) [29]. The combined *BRCA1/2* mutation frequency in a Swedish population of unselected breast cancer cases recruited from 1998 through 2000 in Stockholm has been previously estimated to be not more than 1% in the work by Margolin *et al*. [1]. In that study, screening for *BRCA1* pathogenic variants was limited to exon 11, which covers over half the coding region of *BRCA1* [30]. More than 70% of diagnosed pathogenic variants including four founder pathogenic variants in the Swedish population are known to be located on this exon [31-33]. Prevalence of *BRCA2* pathogenic variants in the Swedish population was deemed by Margolin *et al*. to be negligible among unselected breast cancer patients due to the low frequency of such pathogenic variants even in high-risk groups in the region [1]. On the contrary, only 33 of 50 *BRCA1* pathogenic variants were identified on exon 11 in this study, thus suggesting that 34% of *BRCA1* carriers would have been missed if exon 11 alone were screened. Through testing the entire sequences of *BRCA1/2* genes with improved methodology and techniques, we estimate the combined prevalence of *BRCA1/2* pathogenic variants among unselected breast cancer patients in Sweden to be closer to 2%.

There are close to 2,000 known *BRCA1* germline pathogenic variants, many of which are loss-of-function frameshift pathogenic variants [34]. Nine of 28 (32%) unique *BRCA1* and 6 of 33 (18%) unique *BRCA2* pathogenic variants were found to be recurrent in Swedish breast cancer patients (i.e. pathogenic variants that were found to occur in at least two unrelated individuals). The relatively low recurrent mutation frequency, including that of Swedish founder pathogenic variants, would mean that

screening of selected pathogenic variants alone may not be a sensitive approach in this population as majority of *BRCA1* and *BRCA2* carriers will have been missed. While *BRCA1* pathogenic variants confer a more aggressive tumor phenotype, *BRCA2* pathogenic variants typically resemble sporadic breast cancer [35]. There is good agreement between our observed results regarding the tumor characteristic differences between *BRCA1/2* and non-*BRCA* breast cancer cases and what has been previously reported in literature. It has been observed by others that tumors in *BRCA1* carriers more frequently exhibited high mitotic count, high grade, ER and PR negativity [36-38]. A large proportion of *BRCA1* mutation cases (~80%) have also been documented to be triple negative and basal-like breast cancers [36-38]. In a Swedish study where 54 female breast cancer patients from 22 families with *BRCA2* germ line pathogenic variants from Sweden and Denmark were compared with 214 age- and date of diagnosis-matched controls identified among breast cancer patients from South Sweden, *BRCA2*-associated cases were more often node-positive than non-*BRCA* cases [39]. Other than nodal involvement, *BRCA2*-associated breast carcinomas were generally associated with less aggressive tumor characteristics than *BRCA1* cancers, and were more likely to be hormone-related [37, 38].

Thirty-eight percent of *BRCA1/2* carriers were identified through selective clinical testing of 8.2% of breast cancer patients. Grindedal *et al.* evaluated the results of *BRCA1/2* testing in South-Eastern Norway and found that 65% of the *BRCA1/2* carriers would have been missed if using age of onset below 40 or triple negative breast cancer as criteria for testing [40]. It is also conceivable that, due to an emphasis on disease family history in current guidelines, a smaller family size may compromise the identification of high risk individuals who would otherwise benefit from genetic testing [41]. In a Swedish retrospective study by Nilsson *et al*. where all breast cancer patients were tested, it was found that while 65% of the *BRCA1/2* carriers fulfilled Swedish criteria for testing, only 18% had been identified in regular clinical routine [8]. Other factors such as varying compliance with guidelines for the recommendation of *BRCA* testing by clinicians will lead to even more *BRCA1/2* carriers being missed. It may thus be of benefit to test all newly diagnosed breast cancers in light of available targeted therapy options.

To our knowledge, this is the largest population-based breast cancer testing study for *BRCA1/2* published outside of founder populations. Despite the richness of the data which encompasses patient and tumor, some risk groups were too small to be examined with adequate statistical power (e.g. benign breast disease). The Swedish health care system is mainly government-

funded and decentralized, making it possible to identify all women who went for clinical *BRCA* testing. Nonetheless, private health care also exists, and some *BRCA1/2* carriers may have been identified by commercial testing outside the public sector. However, the number of patients tested outside of the national *BRCA* testing program is likely negligible during the period 2001-2008 [8]. It should be also noted that the Fluidigm Access Array method used cannot detect large rearrangements and has a sensitivity of ~90%, hence further analytical validity studies are needed. More sensitive methods and the universal *BRCA* testing of newly breast cancer patients will help to increase the number of women getting the best treatment for their disease.

In summary, *BRCA1/2* pathogenic variants were found in 1.8% of an unselected Swedish breast cancer cohort. Six out of ten *BRCA* carriers were not identified through selective clinical testing routines. Our results give fruitful information for further decisions of *BRCA* testing for all breast cancer patients at time of diagnosis. The presented data can be a starting point for further studies dealing with issues such as cost effectiveness of screening patients with different tumor characteristics and patient health attitudes.

**FUNDING**

This work was supported by AstraZeneca, the Swedish Research Council (grant no: 2014 -2271 to KC), Swedish Cancer Society (grant no: CAN 2016/684 to KC), FORTE (grant no: 2016-00081 to KC) and ALF Medicine (grant no: 20170088 to KC). This study was also supported by the Cancer Risk Prediction Center (CRisP; www.crispcenter.org), a Linnaeus Centre [grant no: 70867902] financed by the Swedish Research Council. Targeted sequencing was supported by Cancer Research UK grants C1287/A16563 to DFE and C8197/A16565 to AMD, and the PERSPECTIVE project, funded from the Government of Canada through Genome Canada and the Canadian Institutes of Health Research, the *Ministère de l'Économie, de la Science et de l'Innovation du Québec* through Genome Québec, and the Quebec Breast Cancer Foundation. BD was supported by the Intramural Research Program of the National Human Genome Research Institute. JL is a recipient of a Singapore National Research Foundation Fellowship (NRF-NRFF2017-02) and an award from the Alex and Eva Wallström Foundation.

**ACKNOWLEDGEMENTS**

We thank Don Conroy, Caroline Baynes, Patricia Harrington, Martine Dumont and Stéphane Dubois for assistance with the sequencing experiments. We also thank Hanis Mariyah Mohd Ishak and Chek Mei Bok for careful reading of the manuscript.

**FIGURE LEGENDS**

**Figure 1. Mutation plots of *BRCA1*.** Four and three splice variants for *BRCA1* (NM_007294.3) are not shown.

**Figure 2. Mutation plots of *BRCA2*.** Three splice variants for *BRCA2* (NM_000059.3) are not shown.

**Figure 3. Overlap between women attending *BRCA* screening (clinically tested), *BRCA* carriers identified through selective clinical testing routine (clinically-detected carriers), and *BRCA* carriers identified through screening all unselected LIBRO1 breast cancer patients (unselected-detected).** Of the 416 women who were clinically tested, 39 were found to be *BRCA1/2* carriers (39/416, 9.3%). Our study confirmed 35 of these pathogenic variants. Four pathogenic variants were missed (*BRCA1*: c.4186-1785_4358-1667dup and c.4358-1729_4986+736dup; *BRCA2*: c.7805+1538_8331+560del and c.9097_9098insT). By sequencing the entire Swedish study, we found 55 more carriers who were not screened as part of clinical routine.

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**Table 1.** Odds ratio (OR) and corresponding 95% confidence intervals (CI) of predictors according to *BRCA* status.

| | ***BRCA1 vs non-BRCA*** **OR (95% CI)** | ***BRCA2 vs non-BRCA*** **OR (95% CI)** | ***BRCA2 vs BRCA1*** **OR (95% CI)** |
|---|---|---|---|
| *Model 1: Patient characteristics* | | | |
| Age at diagnosis: 50-59 | **0.21 (0.10 to 0.45)** | 0.78 (0.36 to 1.69) | **3.55 (1.05 to 11.97)** |
| Age at diagnosis: ≥60 | **0.14 (0.06 to 0.31)** | 0.55 (0.24 to 1.23) | **3.91 (1.11 to 13.84)** |
| Year of diagnosis: 2005-2008 | 1.68 (0.91 to 3.08) | 1.03 (0.55 to 1.92) | 0.90 (0.33 to 2.48) |
| HRT ever: Yes | 1.08 (0.56 to 2.10 | **0.36 (0.17 to 0.76)** | **0.31 (0.10 to 0.93)** |
| Familiy history of breast cancer: Yes | **3.57 (1.99 to 6.41)** | **2.08 (1.08 to 3.99)** | 0.60 (0.24 to 1.55) |
| Familiy history of ovarian cancer: Yes | **6.99 (3.43 to 14.24)** | **3.57 (1.47 to 8.68)** | 0.38 (0.11 to 1.35) |
| Personal history of ovarian cancer: Yes | **19.21 (5.89 to 62.72)** | **8.01 (1.61 to 39.94)** | 0.49 (0.04 to 6.74) |
| Personal history of any malignant cancer (not breast): Yes | 1.35 (0.52 to 3.54) | 0.81 (0.26 to 2.56) | 0.49 (0.07 to 3.59) |
| | | | |
| *Model 2: Tumor characteristics, adjusted for age and year of diagnosis* | | | |
| Detection mode: Interval | 1.34 (0.38 to 4.79) | 1.16 (0.45 to 3.03) | 0.44 (0.05 to 3.50) |
| Detection mode: Clinical cancer in women without previous mammograms | 2.61 (0.81 to 8.37) | 0.66 (0.20 to 2.12) | 0.35 (0.05 to 2.38) |
| Detection mode: Clinical cancer in women who had previous mammograms (i.e. interval >24 months) | **3.54 (1.15 to 10.89)** | 1.57 (0.63 to 3.94) | 0.34 (0.06 to 2.02) |
| ER status: Negative | **5.19 (2.68 to 10.06)** | 1.17 (0.48 to 2.87) | **0.22 (0.07 to 0.77)** |
| Grade: Intermediate-differentiated | 1.97 (0.24 to 16.23) | 1.82 (0.52 to 6.34) | 1.32 (0.10 to 18.26) |
| Grade: Poorly-differentiated | 7.11 (0.91 to 55.30) | 1.55 (0.39 to 6.22) | 0.36 (0.03 to 4.92) |
| Tumor size: ≥20 | 0.87 (0.48 to 1.59) | 1.26 (0.67 to 2.39) | 1.17 (0.37 to 3.76) |
| Nodal involvement: Yes | 1.60 (0.79 to 3.27) | **2.54 (1.20 to 5.37)** | 1.67 (0.43 to 6.51) |
| | | | |
| *Model 3: Breast cancer subtype, adjusted for age and year of diagnosis* | | | |
| Subtype: Luminal B | 2.83 (0.54 to 14.77) | 0.49 (0.06 to 3.73) | 0.19 (0.01 to 2.60) |
| Subtype: HER2-enriched | 0.93 (0.11 to 8.07) | 0.33 (0.04 to 2.52) | 0.38 (0.02 to 8.07) |
| Subtype: Basal-like | **40.07 (14.26 to 112.59)** | 0.84 (0.11 to 6.43) | **0.02 (0.00 to 0.17)** |

**Table 2. Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of patient characteristics among *BRCA* carriers identified versus not identified through selective clinical screening.**
* Adjusted for year of diagnosis (2001-2004, 2005-2008). † Adjusted for year of diagnosis and gene (*BRCA1*, *BRCA2*). ‡ Adjust for year of diagnosis, gene and age at diagnosis (<50, 50-59, ≥60).

| Patient characteristic | Not identified by selective testing (*n*=57) *n* (%) | Identified by selective testing (*n*=35) *n* (%) | OR (95% CI)* | OR (95% CI)† | OR (95% CI)‡ |
|---|---|---|---|---|---|
| Gene, *unadjusted | | | | | |
| *BRCA1* | 23 (40.4) | 27 (77.1) | 1.00 (Reference) | | |
| *BRCA2* | 34 (59.6) | 8 (22.9) | **0.20 (0.08 to 0.52)** | | |
| Age at diagnosis, *unadjusted | | | | | |
| <50 | 15 (26.3) | 22 (62.9) | 1.00 (Reference) | | |
| 50-59 | 20 (35.1) | 8 (22.9) | **0.27 (0.10 to 0.78)** | | |
| ≥60 | 22 (38.6) | 5 (14.3) | **0.15 (0.05 to 0.50)** | | |
| Year of diagnosis, *unadjusted | | | | | |
| 2001-2004 | 26 (45.6) | 12 (34.3) | 1.00 (Reference) | | |
| 2005-2008 | 31 (54.4) | 23 (65.7) | 1.61 (0.67 to 3.84) | | |
| Education | | | | | |
| University | 29 (50.9) | 21 (60.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Intermediate | 12 (21.1) | 9 (25.7) | 1.06 (0.37 to 2.98) | 1.40 (0.45 to 4.39) | 2.08 (0.59 to 7.40) |
| Elementary | 7 (12.3) | 0 (0.0) | - | - | - |
| Other | 9 (15.8) | 5 (14.3) | 0.78 (0.23 to 2.68) | 0.65 (0.17 to 2.46) | 1.63 (0.35 to 7.66) |
| Age at menarche in years | | | | | |
| <13 | 21 (36.8) | 7 (20.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥13 | 36 (63.2) | 28 (80.0) | 2.17 (0.79 to 5.94) | **2.99 (1.00 to 8.94)** | **4.12 (1.19 to 14.26)** |
| Menopause status before breast cancer diagnosis | | | | | |
| Premenopause | 14 (24.6) | 23 (65.7) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Postmenopause | 43 (75.4) | 12 (34.3) | **0.17 (0.07 to 0.44)** | **0.17 (0.06 to 0.45)** | 0.18 (0.03 to 1.25) |
| BMI in kg/m$^2$ | | | | | |
| <25 | 29 (50.9) | 24 (68.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥25 | 27 (47.4) | 11 (31.4) | 0.52 (0.21 to 1.27) | 0.42 (0.16 to 1.12) | **0.32 (0.11 to 0.94)** |
| Missing | 1 (1.8) | 0 (0.0) | | | |
| Percentage mammographic density | | | | | |
| <25 | 22 (38.6) | 10 (28.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥25 | 16 (28.1) | 14 (40.0) | 1.97 (0.69 to 5.62) | 1.54 (0.51 to 4.69) | 0.93 (0.27 to 3.21) |
| Missing | 19 (33.3) | 11 (31.4) | | | |
| Number of children | | | | | |
| 0 | 12 (21.1) | 3 (8.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| 1 | 13 (22.8) | 7 (20.0) | 2.39 (0.49 to 11.65) | 2.64 (0.50 to 13.83) | 5.34 (0.84 to 33.79) |
| 2 | 22 (38.6) | 14 (40.0) | 2.91 (0.68 to 12.53) | 3.12 (0.68 to 14.24) | 4.76 (0.89 to 25.43) |
| ≥3 | 10 (17.5) | 11 (31.4) | 4.64 (1.00 to 21.66) | 4.69 (0.93 to 23.60) | **10.55 (1.62 to 68.68)** |
| HRT ever | | | | | |
| No | 34 (59.6) | 25 (71.4) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 21 (36.8) | 10 (28.6) | 0.61 (0.24 to 1.54) | 0.45 (0.16 to 1.24) | 0.84 (0.26 to 2.70) |
| Missing | 2 (3.5) | 0 (0.0) | | | |
| Oral contraceptives ever | | | | | |
| No | 19 (33.3) | 5 (14.3) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 37 (64.9) | 30 (85.7) | 3.04 (1.01 to 9.15) | 2.90 (0.91 to 9.24) | 2.36 (0.71 to 7.85) |
| Missing | 1 (1.8) | 0 (0.0) | | | |
| Family history of breast cancer | | | | | |
| No | 37 (64.9) | 18 (51.4) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 20 (35.1) | 17 (48.6) | 1.84 (0.77 to 4.39) | 1.58 (0.63 to 3.99) | 1.46 (0.54 to 3.90) |

| | | | | | |
|---|---|---|---|---|---|
| Family history of ovarian cancer | | | | | |
| No | 50 (87.7) | 24 (68.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 7 (12.3) | 11 (31.4) | **3.11 (1.06 to 9.09)** | 2.87 (0.91 to 9.11) | 3.41 (0.99 to 11.73) |
| Ovarian cancer | | | | | |
| No | 51 (89.5) | 33 (94.3) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 6 (10.5) | 2 (5.7) | 0.60 (0.11 to 3.26) | 0.37 (0.06 to 2.17) | 0.46 (0.07 to 3.01) |
| Other malignant cancer | | | | | |
| No | 48 (84.2) | 31 (88.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 9 (15.8) | 4 (11.4) | 0.76 (0.21 to 2.75) | 0.54 (0.14 to 2.12) | 0.66 (0.15 to 2.96) |

# Prevalence of *BRCA1* and *BRCA2* pathogenic variants in a large, unselected breast cancer cohort

## DATA SUPPLEMENT 1

**eTable 1.** Exclusion criteria for genotyping experiment (Michailidou *et al.* [1]). Of the 5,715 women who consented to genetic analyses of their blood samples, genotyping was successfully performed for 5,125 women. Of these, 5,122 had enough DNA remaining for targeted sequencing.

| **Exclusion criteria for genotyping experiment** | ***n*** |
|---|---|
| Concordant replicate - exclude lower call rate | 116 |
| Cryptic Duplicate | 7 |
| Extreme heterozygous | 34 |
| Call rate (<95%) | 8 |
| Male | 1 |
| Non-European | 114 |
| Phenotype data excluded | 177 |
| Relative pairs with different status | 9 |
| Relative pairs, exclude lower call rate | 39 |
| Unclear whether consented when data released in Jan 2012 | 69 |
| Study duplicates with KARBAC sample | 4 |
| Genotype not received | 12 |

**eMETHODS**

**Details on targeted sequencing methodology used by the University of Cambridge (Fluidigm Access Array method)**

*Targeted sequencing*

Target-enriched sequencing libraries of germline DNA from 5,122 breast cancer patients were prepared at the Centre for Cancer Genetic Epidemiology (University of Cambridge). Data used in this study were part of a larger effort that included samples from other cohorts, as well as coding sequences and intron/exon boundaries for a total of 31 known or suspected breast cancer susceptibility genes, including *BRCA1* and *BRCA2*. Assay design was conducted as previously described [2]. See e**Table 2** (**Data Supplement 2**) for primer sequences and amplicon details.

Briefly, target sequence enrichment was performed using 48.48 Fluidigm Access Arrays according to the manufacturer's protocol (Fluidigm, South San Francisco, California, USA). Fluidigm D3 assay design software was used to select primer pairs, which were multiplexed into pools selected for GC content and avoidance of off-target primer-primer and primer-product complementarity. Target sequences were amplified with Illumina sequencing adaptors and one of 1,536 unique sample barcodes (supplied by Fluidigm, South San Francisco, California, USA). Robotic liquid handling and barcode plate identification were used in all steps of the library preparation process. Each library of amplicons (e**Table 2**, **Data Supplement 2**) for 1,536 samples was quantified with the KAPA Library Quantification Kit (KapaBiosystems, Boston, Massachusetts, USA) and then sequenced on the Illumina Hi-Seq 2500 instrument using v4 chemistry, according to the manufacturer's protocol (Illumina, San Diego, California, USA). Each library was sequenced 2-3 times to provide sufficient coverage.

*Sequence data processing and quality control*

Raw data in *FASTQ* format was received from the University of Cambridge. Paired-end sequencing reads were aligned to the human genome reference sequence (hg19) using Burrows-Wheeler Aligner (version 0.7.12 [3]). Aligned reads in SAM format were converted to BAM format and subsequently merged for each sample using SAMtools (version 1.1 [4]). Read groups were assigned using Picard (version 1.119; http://broadinstitute.github.io/picard). Genome Analysis Toolkit (GATK version 3.7.0; https://software.broadinstitute.org/gatk/) was used for local insertion/deletion (indel) realignment and base quality score recalibration, variant calling, SNP and indel parsing and for deriving quality and depth metrics [5]. The mean read depth across the coding sequences of *BRCA1* and *BRCA2* was 792.2 (standard deviation: 587.4) and 631 (standard deviation: 516), respectively. More than 90% of targeted bases had more than 15x coverage (94.8 [15.9] and 92.5 [20.4] for *BRCA1* and *BRCA2*, respectively).

Genetic variants were called with Unified Genotyper using the default parameters except –mindelFrac 0.05. SNPs and indels with low variant confidence/quality by depth (QD<2) and low approximate read depth (DP<10) were removed. Filter-based annotation of variants were performed using ANNOVAR [6]. A total of 5,099 samples with valid variant calls were included in the final analytical dataset.

**Details on targeted sequencing methodology used by the Department of Oncology, Lund University (modified SureSelect hybrid selection method)**

The clinical mutation screening was performed using the most sensitive methods available for comprehensive detection of all classes of genetic variants known to affect *BRCA1* and *BRCA2*. Targeted sequencing libraries were prepared using a modified SureSelect hybrid selection method and a custom panel targeting 64 genes including complete *BRCA1* and *BRCA2* loci (exons and introns) and 100kb up- and downstream. Specificity was ensured by confirming all variants with Sanger sequencing on an independent DNA extraction from the patient blood sample. Paired-end sequencing of the libraries was performed on a HiSeq 2500 (2x100bp) to an average depth of ~400 reads. Until 2016, this was complemented with multiple ligation-dependent probe amplification (MLPA) for detection of deletions and duplications affecting one or more complete exons. The lab now has validated bioinformatic methods for detecting these variants directly from the sequencing data. Sensitivity estimated using a large collection of positive control samples including all classes of known pathogenic variants is 100%. Before 2010, denaturing high performance liquid chromatography (DHPLC) and MLPA was used. Together, the DHPLC and MLPA have a stated sensitivity of 95%. Many of the samples tested before 2010 have been screened again using the latest methods.

**eTable 3**. Swedish Breast Cancer Group criteria for recommending *BRCA1/2* testing.

| **Criterion** | **Number meeting criterion** |
|---|---|
| Three cases of breast cancer in first degree relatives, or second degree relatives thought a male, with at least one diagnosed ≤50y, and/or ovarian cancer (regardless of age) | 79 |
| Two cases of breast cancer or ovarian cancer in first degree relatives, or second degree relatives thought a male, with at least one case of breast cancer diagnosed ≤40y, or two cases of ovarian cancer (regardless of age) | 113 |
| One case of breast cancer ≤35y | 99 |
| One case of triple-negative breast cancer ≤40y | 20 |
| One case of male breast cancer | NA |
| Breast cancer and ovarian cancer in one individual | 44 |
| Cases of bilateral breast cancer, prostate cancer, and pancreatic cancer may strengthen the indication for screening of pathogenic variants in *BRCA1* and *BRCA2*, but are not defined in any specific criterion | NA |
| Total | 298 |

**eTable 4**. Description of *BRCA1* (NM_007294.3) pathogenic variants.

| Exon | cDNA Change | AA Change | Variant Classification | BIC Nomenclature | Note | *n* |
|---|---|---|---|---|---|---|
| 2 | c.68_69delAG | p.E23fs | frameshift deletion | 185_186delAG,185delAG,187delAG | Founder mutation in Ashkenazi Jews [7] | 3 |
| 5 | c.181T>G | p.C61G | nonsynonymous SNV | 300T>G | Common mutation in Europe [8] | 1 |
| 7 | c.302-2A>G | - | splice site | - | - | 1 |
| 11 | c.930delG | p.Q310fs | frameshift deletion | 1049delG | - | 1 |
| 11 | c.962G>A | p.W321* | stopgain | W321X | - | 1 |
| 11 | c.1082_1092delCAGAGAATCCT | p.S361* | stopgain | 1201del11 | Founder mutation common in Southern Sweden [9] | 5 |
| 11 | c.1360_1361delAG | p.S454* | stopgain | 1479delAG | - | 3 |
| 11 | c.1504_1508delTTAAA | p.L502fs | frameshift deletion | 1623_1627delTTAAA | - | 1 |
| 11 | c.1772delT | p.I591fs | frameshift deletion | 1891delT | - | 1 |
| 11 | c.1961delA | p.K654fs | frameshift deletion | 2080delA | - | 1 |
| 11 | c.2184delA | p.E729fs | frameshift deletion | - | - | 1 |
| 11 | c.2475delC | p.D825fs | frameshift deletion | 2594delC | Swedish BRCA1 founder mutation [10] | 2 |
| 11 | c.3048_3052dupTGAGA | p.N1018fs | frameshift insertion | 3166insTGAGA, p.Asn1018fs | Founder mutation originating from West Coast of Sweden [8, 11] | 8 |
| 11 | c.3178G>T | p.E1060* | stopgain | E1060X | - | 1 |
| 11 | c.3485delA | p.D1162fs | frameshift deletion | 3604delA | Founder mutation in Finland [8] | 1 |
| 11 | c.3607C>T | p.R1203* | stopgain | 3726C>T | - | 1 |
| 11 | c.3626delT | p.L1209* | stopgain | 3745delT | Founder mutation originating in Northern Sweden [8] | 3 |
| 11 | c.3700_3704delGTAAA | p.V1234fs | frameshift deletion | 3819_3823delGTAAA | Frequent mainly in Middle and Eastern Europe and Canada [12] | 1 |
| 11 | c.4035delA | p.E1346fs | frameshift deletion | 4154delA | Common mutation in Poland and Latvia [8] | 2 |
| 13 | c.4201C>T | p.Q1401* | stopgain | - | - | 1 |
| 13 | c.4327C>T | p.R1443* | stopgain | 4446C>T | - | 1 |
| 17 | c.5030_5033delCTAA | p.T1677fs | frameshift deletion | 5149del4,5147del4,5146del4 | - | 1 |
| 18 | c.5075-2A>C | - | splice site | IVS17-2A>C | - | 1 |
| 18 | c.5095C>T | p.R1699W | nonsynonymous SNV | 5214C>T | - | 1 |
| 18 | c.5123C>A | p.A1708E | nonsynonymous SNV | 5242C>A | - | 1 |
| 19 | c.5153-1G>C | - | splice site | IVS18-1G>C | - | 2 |
| 20 | c.5266dupC | p.Q1756fs | frameshift insertion | 5382_5383insC,5382insC,5383insC,5384insC,5385insC | Founder mutation in Russia [13] | 3 |
| 21 | c.5278-2A>T | - | splice site | - | - | 1 |

**eTable 5**. Description of *BRCA2* (NM_000059.3) pathogenic variants.

| Exon | cDNA Change | AA Change | Variant Classification | BIC Nomenclature | Note | *n* |
|---|---|---|---|---|---|---|
| 10 | c.805dupA | p.T269fs | frameshift insertion | 1033insA,p.Thr269fs | - | 1 |
| 10 | c.1310_1313delAAGA | p.K437fs | frameshift deletion | 1537_1540delAAAG | - | 1 |
| 10 | c.1796_1800delCTTAT | p.S599* | stopgain | 2024_2028delCTTAT | - | 1 |
| 10 | c.1813dupA | p.I605fs | frameshift insertion | 2041_2042insA | - | 1 |
| 11 | c.2179delT | p.S727fs | frameshift deletion | - | - | 1 |
| 11 | c.2376C>G | p.Y792* | stopgain | - | - | 1 |
| 11 | c.2476G>T | p.E826* | stopgain | - | - | 1 |
| 11 | c.2578delA | p.I860fs | frameshift deletion | - | - | 1 |
| 11 | c.2808_2811delACAA | p.A938fs | frameshift deletion | 3036_3039delACAA | - | 1 |
| 11 | c.3157_3163delTTAGATA | p.L1053fs | frameshift deletion | - | - | 1 |
| 11 | c.3283C>T | p.Q1095* | stopgain | - | - | 2 |
| 11 | c.3847_3848delGT | p.V1283fs | frameshift deletion | 4075_4076delGT | - | 1 |
| 11 | c.3860delA | p.N1287fs | frameshift deletion | 4088delA,4082delA | - | 1 |
| 11 | c.3950delC | p.T1317fs | frameshift deletion | - | - | 1 |
| 11 | c.5073delA | p.K1691fs | frameshift deletion | 5301delA | - | 3 |
| 11 | c.5754_5755delTA | p.H1918fs | frameshift deletion | - | - | 2 |
| 11 | c.5823delA | p.V1942fs | frameshift deletion | 6051delA | - | 1 |
| 11 | c.5946delT | p.S1982fs | frameshift deletion | 6174delT | Founder mutation in Ashkenazi Jews [8] | 4 |
| 11 | c.6444delT | p.I2149fs | frameshift deletion | - | - | 1 |
| 11 | c.6486_6489delACAA | p.K2162fs | frameshift deletion | 6714_6717delACAA | - | 2 |
| 14 | c.7097dupT | p.T2367fs | frameshift insertion | - | - | 1 |
| 14 | c.7414_7415delAA | p.K2472fs | frameshift deletion | 7642delAA | - | 1 |
| 15 | c.7443delT | p.T2482fs | frameshift deletion | 7671delT | - | 1 |
| 15 | c.7480C>T | p.R2494* | stopgain | 7708C>T | - | 1 |
| 15 | c.7558C>T | p.R2520* | stopgain | 7786C>T | - | 1 |
| 16 | c.7618-1G>A | - | splice site | IVS15-1G>A | - | 1 |
| 17 | c.7974C>G | p.Y2658* | stopgain | Y2658X | - | 1 |
| 19 | c.8332-1G>A | - | splice site | - | - | 1 |
| 20 | c.8513T>G | p.L2838* | stopgain | 8741T>G, p.Leu2838X | - | 1 |
| 22 | c.8910G>A | p.W2970* | stopgain | 9138G>A (W-X),p.Trp2970X | - | 1 |
| 23 | c.9097delA | p.T3033fs | frameshift deletion | - | - | 2 |
| 24 | c.9118-2A>G | - | splice site | IVS23-2A>G | - | 1 |
| 25 | c.9403delC | p.L3135fs | frameshift deletion | 9631delC | - | 1 |

**eTable 6.** Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of patient characteristics according to *BRCA* status. *Adjusted for age (<50, 50-59, ≥60) and year of diagnosis (2001-2004 and 2005-2008).

| **Patient characteristic** | **Non-*BRCA* (*n*=5,007)** | ***BRCA1* (*n*=50)** | ***BRCA2* (*n*=42)** | ***BRCA1* vs non-BRCA OR (95% CI)*** | ***BRCA2* vs non-BRCA OR (95% CI)*** | ***BRCA2* vs BRCA1 OR (95% CI)*** |
|---|---|---|---|---|---|---|
| Age at study entry, years (mean, SD) | 63.4 (9.9) | 54.9 (12.6) | 58.6 (9.4) | | | |
| Age at diagnosis, years (mean, SD) | 58.6 (9.9) | 50.3 (12.4) | 54.0 (9.5) | | | |
| Age at diagnosis, years (unadjusted) | | | | | | |
| <50 | 887 (17.7) | 24 (48.0) | 13 (31.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| 50-59 | 1666 (33.3) | 13 (26.0) | 15 (35.7) | **0.29 (0.15 to 0.57)** | 0.61 (0.29 to 1.30) | 2.13 (0.78 to 5.81) |
| ≥60 | 2454 (49.0) | 13 (26.0) | 14 (33.3) | **0.20 (0.10 to 0.39)** | **0.39 (0.18 to 0.83)** | 1.99 (0.72 to 5.47) |
| Year of diagnosis (unadjusted) | | | | | | |
| 2001-2004 | 2325 (46.4) | 19 (38.0) | 19 (45.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| 2005-2008 | 2682 (53.6) | 31(62.0) | 23 (54.8) | 1.41 (0.80 to 2.51) | 1.05 (0.57 to 1.93) | 0.74 (0.32 to 1.71) |
| Education | | | | | | |
| University | 2113 (42.2) | 29 (58.0) | 21 (50.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Intermediate | 1116 (22.3) | 9 (18.0) | 12 (28.6) | 0.60 (0.28 to 1.27) | 1.09 (0.53 to 2.23) | 1.51 (0.52 to 4.42) |
| Elementary | 753 (15.0) | 3 (6.0) | 4 (9.5) | 0.48 (0.14 to 1.63) | 0.66 (0.22 to 1.96) | 1.10 (0.20 to 6.02) |
| Other | 961 (19.2) | 9 (18.0) | 5 (11.9) | 1.05 (0.48 to 2.29) | 0.63 (0.23 to 1.72) | 0.50 (0.13 to 1.89) |
| Missing | 64 (12.8) | 0 (0.0) | 0 (0.0) | | | |
| Age at menarche, years | | | | | | |
| <13 | 1592 (31.8) | 17 (34.0) | 11 (26.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥13 | 3263 (65.2) | 33 (66.0) | 31 (73.8) | 1.12 (0.62 to 2.03) | 1.52 (0.76 to 3.06) | 1.51 (0.58 to 3.89) |
| Missing | 152 (3.0) | 0 (0.0) | 0 (0.0) | | | |
| BMI, kg/m$^2$ | | | | | | |
| <25 | 2644 (52.8) | 28 (56.0) | 25 (59.5) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥25 | 2275 (45.4) | 22 (44.0) | 16 (38.1) | 1.03 (0.58 to 1.81) | 0.79 (0.42 to 1.49) | 0.84 (0.35 to 2.00) |
| Missing | 88 (1.8) | 0 (0.0) | 1 (2.4) | | | |
| Percentage mammographic density | | | | | | |
| <25 | 2362 (47.2) | 15 (30.0) | 17 (40.5) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥25 | 1507 (30.1) | 20 (40.0) | 10 (23.8) | 1.34 (0.66 to 2.75) | 0.73 (0.32 to 1.65) | 0.52 (0.18 to 1.53) |
| Missing | 1138 (22.7) | 15 (30.0) | 15 (35.7) | | | |
| Number of children | | | | | | |
| 0 | 814 (16.3) | 8 (16.0) | 7 (16.7) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| 1 | 887 (17.7) | 10 (20.0) | 10 (23.8) | 1.26 (0.49 to 3.21) | 1.37 (0.52 to 3.62) | 0.96 (0.24 to 3.85) |
| 2 | 2145 (42.8) | 19 (38.0) | 17 (40.5) | 0.98 (0.43 to 2.26) | 0.96 (0.40 to 2.33) | 0.95 (0.27 to 3.31) |
| ≥3 | 1130 (22.6) | 13 (26.0) | 8 (19.0) | 1.36 (0.56 to 3.31) | 0.89 (0.32 to 2.48) | 0.64 (0.16 to 2.54) |
| Missing | 31 (0.6) | 0 (0.0) | 0 (0.0) | | | |
| HRT ever | | | | | | |
| No | 2208 (44.1) | 30 (60.0) | 29 (69.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 2694 (53.8) | 20 (40.0) | 11 (26.2) | 1.02 (0.53 to 1.94) | **0.36 (0.17 to 0.75)** | 0.36 (0.13 to 1.00) |
| Missing | 105 (2.1) | 0 (0.0) | 2 (4.8) | | | |
| Oral contraceptives ever | | | | | | |
| No | 1285 (25.7) | 11 (22.0) | 13 (31.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 3663 (73.2) | 39 (78.0) | 28 (66.7) | 0.87 (0.43 to 1.75) | 0.58 (0.29 to 1.16) | 0.67 (0.26 to 1.75) |
| Missing | 59 (1.1) | 0 (0.0) | 1 (2.4) | | | |
| Ovarian cancer | | | | | | |
| No | 4971 (99.3) | 44 (88.0) | 40 (95.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 36 (0.7) | 6 (12.0) | 2 (4.8) | **28.02 (10.72 to 73.29)** | **8.11 (1.87 to 35.24)** | 0.27 (0.05 to 1.50) |
| Any malignant cancer, not breast | | | | | | |
| No | 4494 (89.8) | 41 (82.0) | 38 (90.5) | | | |
| Yes | 513 (10.2) | 9 (18.0) | 4 (9.5) | **2.93 (1.37 to 6.27)** | 1.12 (0.39 to 3.20) | 0.39 (0.10 to 1.44) |

| | | | | | | |
|---|---|---|---|---|---|---|
| Family history of breast cancer | | | | | | |
| No | 3948 (78.8) | 27 (54.0) | 28 (66.7) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 916 (18.3) | 23 (46.0) | 14 (33.3) | **4.00 (2.27 to 7.05)** | **2.23 (1.17 to 4.26)** | 0.60 (0.25 to 1.43) |
| Missing | 143 (2.9) | 0 (0.0) | 0 (0.0) | | | |
| Family history of ovarian cancer | | | | | | |
| No | 4753 (94.9) | 38 (76.0) | 36 (85.7) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 231 (4.6) | 12 (24.0) | 6 (14.3) | **7.53 (3.82 to 14.82)** | **3.62 (1.50 to 8.71)** | 0.52 (0.17 to 1.61) |
| Missing | 23 (0.5) | 0 (0.0) | 0 (0.0) | | | |
| Breast cancer in mother | | | | | | |
| No | 4392 (87.7) | 29 (58.0) | 32 (76.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 579 (11.6) | 21 (42.0) | 10 (23.8) | 5.17 (2.92 to 9.17) | 2.29 (1.12 to 4.68) | 0.47 (0.18 to 1.20) |
| Missing | 36 (0.7) | 0 (0.0) | 0 (0.0) | | | |
| Age at breast cancer diagnosis in mother | | | | | | |
| <50 | 92 (15.9) | 11 (52.4) | 4 (40.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥59 | 446 (77.0) | 9 (42.9) | 6 (60.0) | 0.20 (0.08 to 0.50) | 0.37 (0.10 to 1.35) | 2.05 (0.39 to 10.67) |
| Missing | 43 (7.4) | 1 (4.8) | 0 (0.0) | | | |
| Ovarian cancer in mother | | | | | | |
| No | 4822 (96.3) | 39 (78.0) | 36 (85.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 149 (3.0) | 11 (22.0) | 6 (14.3) | 9.82 (4.85 to 19.89) | 5.44 (2.24 to 13.18) | 0.61 (0.20 to 1.86) |
| Missing | 36 (0.7) | 0 (0.0) | 0 (0.0) | | | |
| Ovarian cancer in sister | | | | | | |
| No | 4885 (97.6) | 48 (96.0) | 42 (100.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 86 (1.7) | 2 (4.0) | 0 (0.0) | 3.23 (0.76 to 13.76) | - | - |
| Missing | 36 (0.7) | 0 (0.0) | 0 (0.0) | | | |

**eTable 7.** Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of tumor characteristics according to *BRCA* status. *Adjusted for age (<50, 50-59, ≥60) and year of diagnosis (2001-2004 and 2005-2008).

| **Tumor characteristic** | **Non-*BRCA* (n=5,007) *n* (%)** | ***BRCA1* (n=50) *n* (%)** | ***BRCA2* (n=42) *n* (%)** | ***BRCA1 vs non-BRCA OR (95% CI)**** | ***BRCA2 vs non-BRCA OR (95% CI)**** | ***BRCA2 vs BRCA1 OR (95% CI)**** |
|---|---|---|---|---|---|---|
| Type of breast cancer | | | | | | |
| Invasive | 4470 (89.3) | 48 (96.0) | 42 (100.0) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Non-invasive | 522 (10.4) | 2 (4.0) | 0 (0.0) | 0.37 (0.09 to 1.53) | - | - |
| Missing | 15 (0.3) | 0 (0.0) | 0 (0.0) | | | |
| Detection mode | | | | | | |
| Screen-detected | 1844 (36.8) | 5 (10.0) | 12 (28.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Interval | 768 (15.3) | 5 (10.0) | 7 (16.7) | 2.36 (0.68 to 8.17) | 1.39 (0.54 to 3.54) | 0.63 (0.12 to 3.20 |
| Clinical cancer in women without previous mammograms | 911 (18.2) | 8 (16.0) | 4 (9.5) | **3.99 (1.26 to 12.66)** | 0.76 (0.24 to 2.43) | 0.22 (0.04 to 1.08) |
| Clinical cancer in women who had previous mammograms (i.e. interval >24 months) | 1395 (27.9) | 31 (62.0) | 19 (45.2) | **5.20 (1.78 to 15.15)** | 1.77 (0.73 to 4.29) | 0.35 (0.08 to 1.49) |
| Missing | 89 (1.8) | 1 (2.0) | 0 (0.0) | | | |
| Estrogen receptor status | | | | | | |
| Positive | 3637 (72.6) | 17 (34.0) | 30 (71.4) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Negative | 643 (12.8) | 30 (60.0) | 7 (16.7) | **8.98 (4.90 to 16.46)** | 1.23 (0.54 to 2.82) | **0.14 (0.05 to 0.39)** |
| Missing | 727 (14.5) | 3 (6.0) | 5 (11.9) | | | |
| Progesterone receptor status | | | | | | |
| Positive | 2952 (59.0) | 14 (28.0) | 24 (57.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Negative | 1252 (25.0) | 33 (66.0) | 13 (31.0) | **6.06 (3.21 to 11.46)** | 1.33 (0.67 to 2.63) | **0.23 (0.09 to 0.60)** |
| Missing | 803 (16.0) | 3 (6.0) | 5 (11.9) | | | |
| Grade | | | | | | |
| Well-differentiated | 578 (11.5) | 1 (2.0) | 3 (7.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Moderately differentiated | 1563 (31.2) | 7 (14.0) | 16 (38.1) | 2.41 (0.30 to 19.66) | 1.91 (0.55 to 6.60) | 0.80 (0.07 to 9.47) |
| Poorly differentiated | 822 (16.4) | 31 (62.0) | 9 (21.4) | **17.99 (2.44 to 132.70)** | 1.90 (0.51 to 7.10) | 0.11 (0.01 to 1.22) |
| Missing | 2044 (40.8) | 11 (22.0) | 14 (33.3) | | | |
| Tumor size (mm) | | | | | | |
| <20 | 3020 (60.3) | 27 (54.0) | 23 (54.8) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥20 | 1608 (32.1) | 21 (42.0) | 19 (45.2) | 1.30 (0.73 to 2.32) | 1.47 (0.80 to 2.72) | 1.16 (0.46 to 2.89) |
| Missing | 379 (7.6) | 2 (4.0) | 0 (0) | | | |
| Nodal involvement | | | | | | |
| No | 4503 (89.9) | 39 (78.0) | 32 (76.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 466 (9.3) | 11 (22.0) | 10 (23.8) | **2.08 (1.04 to 4.14)** | **2.71 (1.31 to 5.62)** | 1.27 (0.46 to 3.54) |
| Missing | 38 (0.8) | 0 (0.0) | 0 (0.0) | | | |
| Proliferation level (Ki67) | | | | | | |
| Low (<20%) | 923 (18.4) | 5 (10.0) | 11 (26.2) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| High (≥20%) | 736 (14.7) | 20 (40.0) | 7 (16.7) | **4.25 (1.58 to 11.44)** | 0.72 (0.28 to 1.88) | **0.18 (0.04 to 0.74)** |
| Missing | 3348 (66.9) | 25 (50.0) | 24 (57.1) | | | |
| Molecular subtypes | | | | | | |
| Luminal A | 1212 (24.2) | 5 (10.0) | 15 (35.7) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Luminal B | 156 (3.1) | 2 (4.0) | 1 (2.4) | 2.83 ( 0.54 to 14.77) | 0.49 ( 0.06 to 3.73) | 0.19 (0.01 to 2.60) |
| HER2-enriched | 214 (4.3) | 1 (2.0) | 1 (2.4) | 0.93 ( 0.11 to 8.07) | 0.33 ( 0.04 to 2.52) | 0.38 (0.02 to 8.07) |
| Basal-like | 84 (1.7) | 17 (34.0) | 1 (2.4) | **40.07 (14.26 to 112.59)** | 0.84 ( 0.11 to 6.43) | **0.02 (0.00 to 0.17)** |
| Missing | 3341 (66.7) | 25 (50.0) | 24 (57.1) | | | |

**eTable 8.** Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of tumor characteristics among *BRCA* carriers identified versus not identified through selective clinical screening**.** * Adjusted for year of diagnosis (2001-2004, 2005-2008). † Adjusted for year of diagnosis and gene (*BRCA1*, *BRCA2*). ‡ Adjust for year of diagnosis, gene and age at diagnosis (<50, 50-59, ≥60).

| Tumor characteristic | Not identified by selective testing (*n*=57) *n* (%) | Identified by selective testing (*n*=35) *n* (%) | OR (95% CI)* | OR (95% CI)† | OR (95% CI)‡ |
|---|---|---|---|---|---|
| Type of breast cancer | | | | | |
| Invasive | 56 (98.2) | 34 (97.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Non-invasive | 1 (1.8) | 1 (2.9) | 2.27 (0.13 to 39.73) | 1.11 (0.06 to 20.11) | 1.44 (0.06 to 37.74) |
| Detection mode | | | | | |
| Screen-detected | 14 (24.6) | 3 (8.6) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Interval | 8 (14.0) | 4 (11.4) | 2.56 (0.44 to 14.85) | 2.24 (0.34 to 14.73) | 1.56 (0.21 to 11.33) |
| Clinical cancer in women without previous mammograms | 10 (17.5) | 2 (5.7) | 0.79 (0.11 to 5.72) | 0.41 (0.05 to 3.37) | 0.48 (0.06 to 4.06) |
| Clinical cancer in women who had previous mammograms | 24 (42.1) | 26 (74.3) | **5.52 (1.38 to 22.18)** | 3.85 (0.88 to 16.87) | 1.88 (0.32 to 11.01) |
| Missing | 1 (1.8) | 0 (0.0) | | | |
| Estrogen receptor | | | | | |
| Positive | 34 (59.6) | 13 (37.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Negative | 19 (33.3) | 18 (51.4) | 2.48 (0.99 to 6.19) | 1.29 (0.45 to 3.68) | 0.81 (0.25 to 2.63) |
| Missing | 4 (7.0) | 4 (11.4) | | | |
| Progesterone receptor | | | | | |
| Positive | 25 (43.9) | 13 (37.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Negative | 27 (47.4) | 19 (54.3) | 1.30 (0.53 to 3.19) | 0.69 (0.24 to 1.97) | 0.46 (0.14 to 1.52) |
| Missing | 5 (8.8) | 3 (8.6) | | | |
| Grade | | | | | |
| Poorly-differentiated | 20 (35.1) | 20 (57.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Intermediate-differentiated | 18 (31.6) | 5 (14.3) | **0.28 (0.08 to 0.92)** | 0.48 (0.13 to 1.78) | 0.67 (0.17 to 2.70) |
| Well-differentiated | 4 (7.0) | 0 (0.0) | - | | - |
| Missing | 15 (26.3) | 10 (28.6) | | | |
| Tumor size (mm) | | | | | |
| <20 | 35 (61.4) | 15 (42.9) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| ≥20 | 16 (28.1) | 17 (48.6) | **2.48 (1.00 to 6.16)** | **2.91 (1.07 to 7.92)** | 2.15 (0.74 to 6.24) |
| Missing | 5 (8.8) | 2 (5.7) | | | |
| Nodal involvement | | | | | |
| No | 45 (78.9) | 26 (74.3) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Yes | 12 (21.1) | 9 (25.7) | 1.40 (0.51 to 3.84) | 1.53 (0.52 to 4.52) | 1.15 (0.36 to 3.67) |
| Proliferation level (Ki67) | | | | | |
| Low (<20%) | 11 (19.3) | 5 (14.3) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| High (≥20%) | 12 (21.1) | 15 (42.9) | 2.75 (0.75 to 10.11) | 1.55 (0.37 to 6.43) | 0.80 (0.16 to 3.96) |
| Missing | 34 (59.6) | 15 (42.9) | | | |
| Molecular subtypes | | | | | |
| Luminal A | 14 (24.6) | 6 (17.1) | 1.00 (Reference) | 1.00 (Reference) | 1.00 (Reference) |
| Luminal B | 2 (3.5) | 1 (2.9) | 1.17 (0.09 to 15.46) | 0.65 (0.04 to 9.93) | 0.37 (0.02 to 6.64) |
| HER2-enriched | 2 (3.5) | 0 (0.0) | - | - | - |
| Basal-like | 5 (8.8) | 13 (37.1) | **6.07 (1.49 to 24.76)** | 2.54 (0.52 to 12.41) | 1.49 (0.25 to 8.76) |
| Missing | 34 (59.6) | 15 (42.9) | | | |

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**eTable 2.** Primer sequences and amplicon details. Partially overlapping amplicons were tiled across the target regions with a maximum amplicon length (forward and reverse primer length plus intervening unique sequence) of 200-bp. Primers were designed with melting temperature range 59.0-61.0 ℃. Each primer included an orientation-specific tail sequence for subsequent ligation of adapter and barcode sequences.

| Gene/Chr | Assay Name | Chr | Start | End | Forward primer | Reverse primer | Total amplicon length | GC % | Amplicon | Flag |
|---|---|---|---|---|---|---|---|---|---|---|
| BRCA1 | BRCA1_3_UTR__exon_24__1 | 17 | 41196256 | 41196454 | ACACTGACGACATGGTTCTACAgtgaAAAGGCTCTGAGAAAGTCG | TACGGTAGCAGAGACTTGGTCTGGACTGTTTATAGCTGTTGGAAGGA | 199 | 45 | gtgaAAAGGCTCTGAGAAAGTCGGCTGGCCTAAGTCTCAAGAACAGTCATTCATGGTGGAAGTGTTTGCTACCAAGTTTATTTGCAGTGTTAACAGCACAACATTTACAAAACGTATTTTGTACAATCAAGTCTTCACTGCCCTTGCACACTGGGGGGGGCTAGGGAAGACCTAGTCCTTCCAACAGCTATAAACAGTCC | One primer sits in the repeat region |
| BRCA1 | BRCA1_3_UTR__exon_24__2 | 17 | 41196303 | 41196500 | ACACTGACGACATGGTTCTACACATTCATGGTGGAAGTGTTTGCT | TACGGTAGCAGAGACTTGGTCTTGCTTGCTGAAGGAAGAAAAAGTG | 198 | 41 | CATTCATGGTGGAAGTGTTTGCTACCAAGTTTATTTGCAGTGTTAACAGCACAACATTTACAAAACGTATTTTGTACAATCAAGTCTTCACTGCCCTTGCACACTGGGGGGGCTAGGGAAGACCTAGTCCTTCCAACAGCTATAAACAGTCCTGGATAATGGGTTTATGAGACCTAGTCCTTCCAACAGCTATAAACAGTCCTGGATAATGGGTTTATG | |
| BRCA1 | BRCA1_3UTRB_3 | 17 | 41196422 | 41196600 | ACACTGACGACATGGTTCTACAAGACCTAGTCCTTCCAACAGCTA | TACGGTAGCAGAGACTTGGTCTAAATGACAGATCCCACCAGGAAG | 179 | 39 | AAAAACACTTTTTCTTCCTTCAGCAAGCAAAATTATTTATGAAGCTGTATGGTTTCAGCAACAGGGAGCAAAGGAAAAAAATCACCTCAAAGAAAGCAACAGCTTCCTTCCTGGTGGGATCTGTCATTT | |
| BRCA1 | BRCA1_3UTRB_4 | 17 | 41196516 | 41196686 | ACACTGACGACATGGTTCTACACTGTATGGTTTCAGCAACAGGGA | TACGGTAGCAGAGACTTGGTCTAGTAAAATGTTTATTGTTGTAGCTCTGG | 171 | 36 | CTGTATGGTTTCAGCAACAGGGAGCAAAGGAAAAAAATCACCTCAAAGAAAGCAACAGCTTCCTTCCTGGTGGGATCTGTCATTTATTCATGCCAGAGGTCTTATATTTTAAGAGGAATGGATTATATACCAGAGCTACAACAATAAACATTTTACT | |
| BRCA1 | BRCA1_3_UTR__exon_24__5 | 17 | 41196609 | 41196779 | ACACTGACGACATGGTTCTACATGAAATATTCATGCCAGAGGTCTT | TACGGTAGCAGAGACTTGGTCTTTTGCTAGATTTCTAAAGAATGTGTTCTAA | 171 | 31 | TGAAATATTCATGCCAGAGGTCTTATATTTTAAGAGGAATGGATTATATACCAGAGCTACAACAATAAACATTTTACTTATTACTAATGAGGAATTAGAAGACTGTCTTTGGAAACCGGTTCTTGAAAATCTTCTGCTGTTTTAGAACACATTCTTTAGAAATCTAGCAAA | |
| BRCA1 | BRCA1_3_UTR__exon_24__6 | 17 | 41196796 | 41196982 | ACACTGACGACATGGTTCTACAAGAAATCTCTTCTAGTTTCATTTTCCTTT | TACGGTAGCAGAGACTTGGTCTCGGTCATGGTGGTGGACA | 187 | 49 | AGAAATCTCTTCTAGtttcattttccttttttttttttttttttgagccacagtctcactgtcacccaggctggagtgccgtggtatgatcttggctcactgcaacctccacctcccgggctgaagtgattctcctgcctagccacctgagtagctgggattacaggtgtccaccaccatgaccg | Two primers sits in the repeat region |
| BRCA1 | BRCA1_3_UTR__exon_24__7 | 17 | 41196962 | 41197133 | ACACTGACGACATGGTTCTACAAGGTGTCCACCACCATGA | TACGGTAGCAGAGACTTGGTCTAAGGAAACTTGAAACCTGGGCAT | 172 | 52 | aggtgtccaccaccatgaccggctaatttctgtatttttagtagagatgggggtttcaccatgttggccaggctggtttcgaactcctgacctccagtgatctgcccaccttggcctcccaaagtgctgggattacaggcgtgagccaccatgcccagGTTTCAAGTTTCCTTT | Two primers sits in the repeat region |
| BRCA1 | BRCA1_3_UTR__exon_24__8 | 17 | 41197109 | 41197273 | ACACTGACGACATGGTTCTACAccatgcccagGTTTCAAGTTT | TACGGTAGCAGAGACTTGGTCTGCAGAGAGTCAGACCCTTCAAT | 165 | 45 | ccatgcccagGTTTCAAGTTTCCTTTTCATTTCTAATACCTGCCTCAGAATTTCCTCCCCAATGTTCCACTCCAACATTTGAGAACTGCCCAAGGACTATTCTGACTTTAAGTCACATAATCGATCCCAAGCACTCTCCTTCCATTGAAGGGTCTGACTCTCTGC | One primer sits in the repeat region |
| BRCA1 | BRCA1_3_UTR__exon_24__9 | 17 | 41197192 | 41197381 | ACACTGACGACATGGTTCTACAAACTGCCCAAGGACTATTCTGAC | TACGGTAGCAGAGACTTGGTCTTCTATTCAGGCTGTTGTTGGCTT | 190 | 46 | AACTGCCCAAGGACTATTCTGACTTTAAGTCACATAATCGATCCCAAGCACTCTCCTTCCATTGAAGGGTCTGACTCTCTTCCAGTTTAGAGAAGTAAACTTAGGGAAACCAGCTATTCTCTTGAGGCCAAGCCACTCTGTGCTTCCAGCCCTAAGCCAACAACAGCCTGAATAGA | |
| BRCA1 | BRCA1_3_UTR__exon_24__10 | 17 | 41197309 | 41197497 | ACACTGACGACATGGTTCTACAGGGAAACCAGCTATTCTCTTGAGG | TACGGTAGCAGAGACTTGGTCTGGAAATCTGCCATGAGCACAAAA | 189 | 41 | GGGAAACCAGCTATTCTCTTGAGGCCAAGCCACTCTGTGCTTCCAGCCCTAAGCCAACAACAGCCTGAATAGAAAGAATAGGGCTGATAAATAATGAATCAGCATCTTGCTCAATTGGTGGCGTTTAAATGGTTTTAAAATCTTCTCAGGTGAAAAATTACCATAATTTTGTGCTCATGGCAGATTTCC | |
| BRCA1 | BRCA1_3_UTR__exon_24__11 | 17 | 41197360 | 41197558 | ACACTGACGACATGGTTCTACAAGCCAACAACAGCCTGAATAGAA | TACGGTAGCAGAGACTTGGTCTCTGAAAAGGACTTCTGGCTATGC | 199 | 39 | AGCCAACAACAGCCTGAATAGAAAGAATAGGGCTGATAAATAATGAATCAGCATCTTGCTCAATTGGTGGCGTTTAAATGGTTTTAAAATCTTCTCAGGTGAAAAATTACCATAATTTTGTGCTCATGGCAGATTTCCAAGGGAGACTTCAAGCAGAAAATCTTTAAGGGACCCTTGCAGAGTTTCCAAGGGAGACTTCAAGCAGAAAATCTTTAAGGGACCCTTG | |
| BRCA1 | BRCA1_3_UTR__exon_24__12 | 17 | 41197488 | 41197682 | ACACTGACGACATGGTTCTACAGCAGATTTCCAAGGGAGACTTCA | TACGGTAGCAGAGACTTGGTCTACAGGTACAGAGCCACAGGA | 195 | 48 | CATAGCCAGAAGTCCTTTTCAGGCTGATGTACATAAAATATTTAGTAGCCAGGACAGTAGAAGGACTGAAGAGTGAGAGGAGCTCCCAGGGCCTGGAAAGGCCACTTTGTAAGCTCATTCTTGGGGTCCTGTGGCTCTGTACCTGTTAGCCAGGACAGTAGAAGGACTGAAGAGTGAGAGGAGCTCCCAGGGCCTGGAAAGGCCACTTTGTAAGCTCATTCTTGGGGTCCTGTGGCTCTGTAC | |
| BRCA1 | BRCA1_3UTRA_3 | 17 | 41197582 | 41197779 | ACACTGACGACATGGTTCTACATAGCCAGGACAGTAGAAGGACTG | TACGGTAGCAGAGACTTGGTCTGTGGGTGTTGGACAGTGTAGC | 198 | 57 | CTGTGGCTGGCTGCAGTCAGTAGTGGCTGTGGGGGATCTGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACACTGTCCAACACCCAC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_1 | 17 | 41197714 | 41197895 | ACACTGACGACATGGTTCTACAATCTGGGGTATCAGGTAGGTGTC | TACGGTAGCAGAGACTTGGTCTCCTGGAGTCGATTGATTAGAGCC | 182 | 52 | ATCTGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTGCCTCACACATCTGCCCAATTGCTGGAGACAGAGAACACAAGCAGAGATTAGTGTCAATTCATTCTCCTGGACTAGGCTCTAATCAATCGACTCCAGG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_2 | 17 | 41199563 | 41199750 | ACACTGACGACATGGTTCTACATGCCAAGAACTGTGCTACTCAAG | TACGGTAGCAGAGACTTGGTCTTTGAATGCTCTTTCCTTCCTGGG | 188 | 51 | tgccaagaactgtgctactcaagcaccaggtaatgagtgataaaccaaacccatgcaaaagGACCCCATATAGCACAGGTACATGCAGGCACCTTACCATGGAAGCCATTGTCCTCTGTCCAGGCATCTGGCTGCACAACCACAATTGGGTGGACACCCTGGATCCCCAGGAAGGAAAGAGCATTCAA | One primer sits in the repeat region |
| BRCA1 | BRCA1_3 | 17 | 41201071 | 41201269 | ACACTGACGACATGGTTCTACAGGTGCCAGTCTTGCTCACAG | TACGGTAGCAGAGACTTGGTCTGGCCTGGGTTAAGTATGCAGAT | 199 | 47 | GGTGCCAGTCTTGCTCACAGGAGAGAATATTGTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGACATTTAGATGTAAAATCACTGCAGTAATCTGCATACTTAACCCAGGCC | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| BRCA1 | BRCA1_4 | 17 | 41202996 | 41203184 | ACACTGACGACATGGTTCTACACCCATCGTGGGATCTTGCTTAT | TACGGTAGCAGAGACTTGGTCTTTTTCCTTCTCTCCATTCCCCTG | 189 | 51 | CCCATCGTGGGATCTTGCTTATAATACTCCACTATGTAAGACAAAGGCTGGTGCTGGAACTCTGGGGTTCTCCCAGGCTCTTACCTGTGGGCATGTTGGTGAAGGGCCCATAGCAACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAGGAAGAGAGAGGGACAGGGGAATGGAGAGAAGGAAAA |
| BRCA1 | BRCA1_5 | 17 | 41208999 | 41209195 | ACACTGACGACATGGTTCTACACTCTGCAAAGGGGAGTGGAATAC | TACGGTAGCAGAGACTTGGTCTTCTCTTTCTCTTATCCTGATGGGT | 197 | 46 | CTCTGCAAAGGGGAGTGGAATACAGAGTGGTGGGGTGAGATTTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGGGATTCTCTTGCTCGCTTTTGGACCTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGACTTCAAAATCATGCTGAAAGAAACCAAACACAACCCATCAGGATAAGAGAAAGAGA |
| BRCA1 | BRCA1_6 | 17 | 41215258 | 41215442 | ACACTGACGACATGGTTCTACAGAAAGTGGTGCATTGATGGAAGG | TACGGTAGCAGAGACTTGGTCTAAGAGCACGTTCTTCTGCTGTAT | 185 | 36 | GAAAGTGGTGCATTGATGGAAGGAAGCAAATACATTTTTAACTATATGACTGAATGAATATCTCTGGTTAGTTTGTAACATCAAGTACTTACCTCATTCAGCATTTTTCTTTCTTTAATAGACTGGGTCACCCCTAAAGAGATCATAGAAAAGACAGGTTACATACAGCAGAAGAACGTGCTCTT |
| BRCA1 | BRCA1_7 | 17 | 41215830 | 41216019 | ACACTGACGACATGGTTCTACAGGTGTAAAAATGCAATTCTGAGGTGT | TACGGTAGCAGAGACTTGGTCTTCCTGATTTTGTTTTCAACTTCTAATCC | 190 | 37 | GGTGTAAAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACCCATTTTCCTCCCGCAATTCCTAGAAAATATTTCAGTGTCCGTTCACACACAAACTCAGCATCTGCAGAATGAAAAACACTCAAAGGATTAGAAGTTGAAAACAAAATCAGGA |
| BRCA1 | BRCA1_8 | 17 | 41219582 | 41219777 | ACACTGACGACATGGTTCTACATATGCAGCAGATGCAAGGTATTC | TACGGTAGCAGAGACTTGGTCTAACTAGTATTCTGAGCTGTGTGC | 196 | 35 | TATGCAGCAGATGCAAGGTATTCTGTAAAGGTTCTTGGTATACCTGTTTTCATAACAACATGAGTAGTCTCTTCAGTAATTAGATTAGTTAAAGTGATGTGGTGTTTTCTGGCAAACTTGTACACGAGCATCTGAAATTAAATCAAATATTCCATTATCATGAGTTACCTCTAGCACACAGCTCAGAATACTAGTT |
| BRCA1 | BRCA1_Intron_16_1 | 17 | 41220845 | 41221039 | ACACTGACGACATGGTTCTACACGTAAGAAGGCTTAGAAGGGGTTC | TACGGTAGCAGAGACTTGGTCTTGGCTAGTAAATGATGGCCCTTG | 195 | 37 | CGTAAGAAGGCTTAGAAGGGGTTCATGTTCTTCCCCAAAGAAATTTAGAGTCCTCTAGCTATTATCTATCAACCAAATAAAAATCAATAGGCAGCAAAAGAAATTAACCAGATCAATTATGGGCACAGTTGACCTAGCTGGTAGGTATT |
| BRCA1 | BRCA1_Intron_16_2 | 17 | 41220960 | 41221131 | ACACTGACGACATGGTTCTACAATTATGGGCACAGTTGACCTAGC | TACGGTAGCAGAGACTTGGTCTAGTATGGAGTGAGGCAACATGAA | 172 | 44 | GTCTGATAAATAACTTTGTTTACCAAGGGCCATCATTTACTAGCCAATTATGGGCACAGTTGACCTAGCTGGTAGGTATTGTCTGATAAATAACTTTGTTTACCAAGGGCCATCATTTACTAGCCACAGTATTTACGTGTTGCACAATACTGCCATGAAGGTCAGGCCATCTTTCTTTTCATGTTGCCTCACTCCATACT |
| BRCA1 | BRCA1_Intron_16_3 | 17 | 41221006 | 41221202 | ACACTGACGACATGGTTCTACAACTTTGTTTACCAAGGGCCATCA | TACGGTAGCAGAGACTTGGTCTCGGAGGGTGGTAGCAAAAGG | 197 | 49 | ACTTTGTTTACCAAGGGCCATCATTTACTAGCCATAGCCACAGCCACTCACACCAGTATTTACGTGTTGCACAATACTGCCATGAAGGTCAGGCCATCTTTCTTTCATGTTGCCTCACTCCATACTGCCACAGGGCACTGAAAAAAGGCAGGCTAGAGAAGCTAATGACATCCTCCCCCTTTTGCTACCAGGCTCTGAAACTGTTCAGTTAGAAGAGCAATGCTGAACTGCTGAA |
| BRCA1 | BRCA1_Intron_16_4 | 17 | 41221097 | 41221291 | ACACTGACGACATGGTTCTACAGGCCATCTTTCTTTCATGTTGCC | TACGGTAGCAGAGACTTGGTCTTTCAGCAGTTCAGCATTGCTCTT | 195 | 47 | AAAAAAGGCAGGCTAGAGAAGCTAATGACATCCTCCCCCTTTTGCTACCACCCTCCGCCAGGATCATTAGCAATTCTGAACTGATTAATTGCTGAAATCCCAGCCTTGAAACTGTTCAGTTAGAAGAGCAATGCTGAACTGCTGAAAACTCTTTCCAGAATGTTGTTAAGTCTTAGTCATTAGGGAGATACATATG |
| BRCA1 | BRCA1_9 | 17 | 41222884 | 41223082 | ACACTGACGACATGGTTCTACAAACTCTTTCCAGAATGTTGTTAAGTC | TACGGTAGCAGAGACTTGGTCTGCTCATACTACTGATACTGCTGGG | 199 | 43 | GATACACTCACAAATTCTTCTGGGGTCAGGCCAGACACCACCATGGACATTCTTTTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_10 | 17 | 41222991 | 41223181 | ACACTGACGACATGGTTCTACATTGACCCTTTCTGTTGAAGCTGT | TACGGTAGCAGAGACTTGGTCTGCCCCAGAGTCAGCTCGT | 191 | 48 | TTCTTCCATTGCATTATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAGAGGTTGAAGATGGTATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAGAGGTTGAAGATGGTAT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_11 | 17 | 41223105 | 41223287 | ACACTGACGACATGGTTCTACATCTGCAACTTTCAATTGGGGAAC | TACGGTAGCAGAGACTTGGTCTTGTGTAAATTAAACTTCTCCCATTCCT | 183 | 46 | GTTGCCAACACGAGCTGACTCTGGGGCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATTCCAGATTCCAGGTAAGGGGTTCCCCTCTGAAAGGAATGGGAGAAGTTTAATTTACACA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_12 | 17 | 41226290 | 41226486 | ACACTGACGACATGGTTCTACAATGTAGGATTCAGAGTAAAATCAAAGTG | TACGGTAGCAGAGACTTGGTCTTGCTCTGGGAGTCTTCAGAATAGA | 197 | 43 | ATGTAGGATTCAGAGTAAAATCAAAGTGTTTGTTCCAATACAGCAGATGAAATATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTGGCCCAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTGAAGACTCCCAGAGCA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_13 | 17 | 41226396 | 41226580 | ACACTGACGACATGGTTCTACACAGACTCTTCCAGCTGTTGCT | TACGGTAGCAGAGACTTGGTCTCAATTGGTGGCGATGGTTTTCTC | 185 | 45 | CAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTGAAGACTCCCAGAGCAACTGTGCATGTACCACCTATCATCTAATGATGGGCATTTAGAAGGGGATGACCTAGAAAGATAAATGGAAGGAGAAAACCATCGCCACCAATTG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_14 | 17 | 41228395 | 41228576 | ACACTGACGACATGGTTCTACATGCCTGTATGCAAAAAACTGGAG | TACGGTAGCAGAGACTTGGTCTCCTTTCTGCTGACAAGTTTGAGG | 182 | 35 | TGCCTGTATGCAAAAAACTGGAGAAAGTATGGTGAAAAAAATTAACAATCAGAGTTCAATATAAATAAAGATGTCAGATACCACAGCATCTTTACATTGATGTTTCTTACCTTTCCACTCCTGGTTCTTTATTTTTACTGGTAGAACTATCTGCAGACACCTCAAACTTGTCAGCAGAAAGG |
| BRCA1 | BRCA1_15 | 17 | 41228496 | 41228684 | ACACTGACGACATGGTTCTACAGTTTCTTACCTTTCCACTCCTGGT | TACGGTAGCAGAGACTTGGTCTTCACTATCAGAACAAAGCAGTAAAGT | 189 | 37 | GTTTCTTACCTTTCCACTCCTGGTTCTTTATTTTTACTGGTAGAACTATCTGCAGACACCTCAAACTTGTCAGCAGAAAGGCCTTCTGGATTCTGGCTTATAGGGTATTCACTACTTTTCTGTGAAGTTAATACTGCTTTAAATGGAATGAGAAAACAAATCTACTTTACTGCTTTGTTCTGATAGTGA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_16 | 17 | 41231286 | 41231459 | ACACTGACGACATGGTTCTACAGCCAGAACCACCATCTTTCAGTA | TACGGTAGCAGAGACTTGGTCTAGTACCCGTTCCCTTGATGTCTA | 174 | 42 | GCCAGAACCACCATCTTTCAGTAATTTGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCACCTGATATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCATGTATATGCGAATCTGTAAGAAAGGTGAAATTGTAGACATCAAGGGAACGGGTACT |
| BRCA1 | BRCA1_Intron_13_1 | 17 | 41231398 | 41231595 | ACACTGACGACATGGTTCTACATGGCCATGTATATGCGAATCTGT | TACGGTAGCAGAGACTTGGTCTTCAATACGCACATTAATTCTCTTGGC | 198 | 43 | TGGCCATGTATATGCGAATCTGTAAGAAAGGTGAAATTGTAGACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAAAAGTCTACAACGTGACCCAGCATGCTGTTGGCATCGCTGTAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGTGCGTATTGA |
| BRCA1 | BRCA1_Intron_13_2 | 17 | 41231492 | 41231689 | ACACTGACGACATGGTTCTACATGGCAAAACTGGAAAAGTCTACA | TACGGTAGCAGAGACTTGGTCTCCACGTACCTTTCTCTTTGGCTT | 198 | 43 | TGGCAAAACTGGAAAAGTCTACAACGTGACCCAGCATGCTGTTGGCATCGCTGTAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGTGCGTATTGAGCACATTAAACACTCTAAGAGCCAAGACAGCTTCCTGAAACGC |

Assays designed by relax mode and have no off-target hits

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| BRCA1 | BRCA1_Intron_13_3 | 17 | 41231596 | 41231778 | ACACTGACGACATGGTTCTACAGCACATTAAACACTCTAAGAGCCAA | TACGGTAGCAGAGACTTGGTCTGGAATAGGTTCCAGCTGCTCA | 183 | 48 | GTGAAGGAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACGTGG<br>GCACATTAAACACTCTAAGAGCCAAGACAGCTTCCTGAAACGCGTGAAG<br>GAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACGTGGGTTC<br>AACTGAAGCACCAGCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAAC<br>CAATGGGAAGGAGCCTGAGCAGCTGGAACCTATTCC<br>CAAAGAGAAAGGTACGTGGGTTCAACTGAAGCACCAGCCTGCTCCACC |
| BRCA1 | BRCA1_Intron_13_4 | 17 | 41231671 | 41231869 | ACACTGACGACATGGTTCTACACAAAGAGAAAGGTACGTGGGTTC | TACGGTAGCAGAGACTTGGTCTTGTTCTGGTGATAGAATGACTTTTCTT | 199 | 41 | CAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCAGCT<br>GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAAAAAA<br>AAAAAGACCTTTGGACTGTAAAAAAAAAGAAAAGTCATTCTATCACCAGAACA |
| BRCA1 | BRCA1_Intron_13_5 | 17 | 41231760 | 41231936 | ACACTGACGACATGGTTCTACAAGCAGCTGGAACCTATTCCCTAT | TACGGTAGCAGAGACTTGGTCTACACAAGGCTTAGGTTGGGCTTCAT | 177 | 32 | AGCAGCTGGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAA<br>AAAAAAAAAAAAGACCTTTGGACTGTAAAAAAAAAGAAAAGTCATTCTAT<br>CACCAGAACATTTAGCATATAAATTCCTCTTCTTACTACAATGGGCCTCA<br>TGCAATGAAGCAAATAAGATAACTTGT |
| BRCA1 | BRCA1_Intron_13_6 | 17 | 41231851 | 41232048 | ACACTGACGACATGGTTCTACATCATTCTATCACCAGAACATTTAGCA | TACGGTAGCAGAGACTTGGTCTCACAAGGCTTAGGTTGGGCTT | 198 | 35 | TCATTCTATCACCAGAACATTTAGCATATAAATTCCTCTTCTTACTACAAT<br>GGGCCTCATGCAATGAAGCAAATAAGATAACTTGTTAGAAGTTAACAACT<br>CAATAGAACCTGAAAAACAGAGCAAAACCTTTCTGCTTTTTTTTCTCCTTA<br>ATCCTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTG |
| BRCA1 | BRCA1_Intron_13_7 | 17 | 41231905 | 41232081 | ACACTGACGACATGGTTCTACACCTCATGCAATGAAGCAAATAAGAT | TACGGTAGCAGAGACTTGGTCTTTCCTAAACCAGCCAGCAAGTAG | 177 | 37 | CCTCATGCAATGAAGCAAATAAGATAACTTGTTAGAAGTTAACAACTCAA<br>TAGAACCTGAAAAACAGAGCAAAACCTTTCTGCTTTTTTTTCTCCTTAATC<br>CTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTGACATGAT<br>GATCTACTTGCTGGCTGGTTTAGGAA |
| BRCA1 | BRCA1_Intron_13_8 | 17 | 41232004 | 41232201 | ACACTGACGACATGGTTCTACATCCTTAATTCATTCTCTGAACAGCA | TACGGTAGCAGAGACTTGGTCTTGGCCCATACTTCCTATCCACAA | 198 | 39 | TCCTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTGACATG<br>ATGATCTACTTGCTGGCTGGTTTAGGAAAGTCTAAATGCAGAGATCCAG<br>AGTCCAAGTTTCAGAATATTATTGTAGTTCCTCTTAAATCATTCCCTCATC<br>TAGATGTCTTAACATGTTACATTCTTTGTGGATAGGAAGTATGGGCCA |
| BRCA1 | BRCA1_17 | 17 | 41234313 | 41234511 | ACACTGACGACATGGTTCTACAGAGCAAGGATCATAAAATGTTGGAG | TACGGTAGCAGAGACTTGGTCTAGCCAGCCTTCTAACAGCTAC | 199 | 43 | GAGCAAGGATCATAAAATGTTGGAGCTAGGTCCTTACTCTTCAGAAGGA<br>GATAAAGGGGAAGGAAAGAATTTTGCTTAAGATATCAGTGTTTGGCCAA<br>CAATACACACCTTTTTCTGATGTGCTTTGTTCTGGATTTCGCAGGTCCTC<br>AAGGGCAGAAGAGTCACTTATGATGGAAGGGTAGCTGTTAGAAGGCTG<br>GCT |
| BRCA1 | BRCA1_18 | 17 | 41234442 | 41234625 | ACACTGACGACATGGTTCTACACTGGATTTCGCAGGTCCTCAAG | TACGGTAGCAGAGACTTGGTCTTCATTTTCTTGGTGCCATTTATCGT | 184 | 46 | CTGGATTTCGCAGGTCCTCAAGGGCAGAAGAGTCACTTATGATGGAAGG<br>GTAGCTGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTAGT<br>TCAGCCATTTCCTGCTGGAGCTTTATCAGGTTATGTTGCATGGTATCCCT<br>CTGCTTCAAAAACGATAAATGGCACCAAGAAAATGA |
| BRCA1 | BRCA1_Intron_12__region_2__1 | 17 | 41236576 | 41236770 | ACACTGACGACATGGTTCTACAACTCTCCGTTTCTTCTTCTGATCC | TACGGTAGCAGAGACTTGGTCTAATGGCATTGCTGCAGACCTT | 195 | 40 | ACTCTCCGTTTCTTCTTCTGATCCTTAAAAATGACTTTGCCCTTTACTAAA<br>AACAAGCCATCTTCTTTCTCCTGCTACACTGAGTTCACAATTTTCAGGAG<br>GTTTTTATGACCAGAAAATGTATTCCTAGCTTCACAAAGGTTTCTACTGCT<br>ACTCTAACACTGCTTTGCTGCCAAGGTCTGCAGCAATGCCATT |
| BRCA1 | BRCA1_Intron_12__region_2__2 | 17 | 41236708 | 41236884 | ACACTGACGACATGGTTCTACATCACAAAGGTTTCTACTGCTACTCT | TACGGTAGCAGAGACTTGGTCTCCTGTGAAGCATTTTGGTCAGAT | 177 | 46 | TCACAAAGGTTTCTACTGCTACTCTAACACTGCTTTGCTGCCAAGGTCTG<br>CAGCAATGCCATTGCCACCACGTGGTACTCGTGAGTAGTTACATCACTG<br>ATCAAACCCTAGCCAAAGTCTTGCCTCAGTCAACCTGGAATGAAAGCAC<br>ATAGATATCTGACCAAAATGCTTCACAGG |
| BRCA1 | BRCA1_Intron_12__region_2__3 | 17 | 41236803 | 41236999 | ACACTGACGACATGGTTCTACAACTGATCAAACCCTAGCCAAAGT | TACGGTAGCAGAGACTTGGTCTTTGGGAAACCCAAAGGAAAGTTA | 197 | 40 | ACTGATCAAACCCTAGCCAAAGTCTTGCCTCAGTCAACCTGGAATGAAA<br>GCACATAGATATCTGACCAAAATGCTTCACAGGCTGTATTAGTCACTACT<br>GTCACAACCATCACATCTAACCTCTACGTGGCCATTACATAAATCAGAAA<br>AAGTAGTGGGGTAATTATTAATAGATAACTTTCCTTTGGGTTTCCCAA |
| BRCA1 | BRCA1_Intron_12__region_1__1 | 17 | 41237464 | 41237643 | ACACTGACGACATGGTTCTACATGCCATTAGGATAAAATTCCTCAACA | TACGGTAGCAGAGACTTGGTCTAAAAGAGGAGTGGCAGCAAGTAA | 180 | 41 | TGCCATTAGGATAAAATTCCTCAACATAGCATTCAAAAGGCCCTTTATAC<br>CCTGGTATTATCTCTCATTTCTCCCAACACCCCTCACACAAGTTGTTTTC<br>CTATAACACATGACAACTTTACGTTTCCTGGGAATTCCATGACTCTGTAC<br>CTTTACCTTACTTGCTGCCACTCCTCTTTT |
| BRCA1 | BRCA1_Intron_12__region_1__2 | 17 | 41237543 | 41237725 | ACACTGACGACATGGTTCTACACCCCTCACACAAGTTGTTTTCCT | TACGGTAGCAGAGACTTGGTCTTCATATTTCACAACTCCTCCTGGT | 183 | 42 | CCCCTCACACAAGTTGTTTTCCTATAACACATGACAACTTTACGTTTCCT<br>GGGAATTCCATGACTCTGTACCTTTACCTTACTTGCTGCCACTCCTCTTT<br>TTCCACTTGGAAAAATTCTCATCTTTCAAGGCCTAGTTTGAATGTCTCCTT<br>AAGTCCCCACCAGGAGGAGTTGTGAAATATGA |
| BRCA1 | BRCA1_Intron_12__region_1__3 | 17 | 41237628 | 41237825 | ACACTGACGACATGGTTCTACACTGCCACTCCTCTTTTTCCACT | TACGGTAGCAGAGACTTGGTCTTATACACTCTGCTTCCCTCCAGA | 198 | 46 | CTGCCACTCCTCTTTTTCCACTTGGAAAAATTCTCATCTTTCAAGGCCTA<br>GTTTGAATGTCTCCTTAAGTCCCCACCAGGAGGAGTTGTGAAATATGAG<br>AAGTAAGGGCAAGTGGGCAGAATGTGGCTAATTCTAATAAGACTCCTGA<br>AATGTGCAGCAGAGCAGCCGGAACTGGTCTGGAGGGAAGCAGAGTGTA<br>TA |
| BRCA1 | BRCA1_Intron_12__region_1__4 | 17 | 41237700 | 41237896 | ACACTGACGACATGGTTCTACACCACCAGGAGGAGTTGTGAAATA | TACGGTAGCAGAGACTTGGTCTATACACATGTTTTATGGGAAGGTTTT | 197 | 41 | CCACCAGGAGGAGTTGTGAAATATGAGAAGTAAGGGCAAGTGGGCAGA<br>ATGTGGCTAATTCTAATAAGACTCCTGAAATGTGCAGCAGAGCAGCCGG<br>AACTGGTCTGGAGGGAAGCAGAGTGTATATCTGACCCTTGTTTGTTCAC<br>ATTCATTACATATAAATATATATATAAAACCTTCCCATAAAACATGTGTAT |
| BRCA1 | BRCA1_19 | 17 | 41242903 | 41243101 | ACACTGACGACATGGTTCTACACTACTGAATGCAAAGGACACCAC | TACGGTAGCAGAGACTTGGTCTGCAGCGTTTATAGTCTGCTTTTAC | 199 | 45 | CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACACACACAC<br>GCTTTTTACCTGAGTGGTTAAAATGTCACTCTGAGAGGATAGCCCTGAG<br>CAGTCTTCAGAGACGCTTGTTTCACTCTCACACCCAGATGCTGCTTCAC<br>CTTAAATAACAAAAACAGAGGTTCAGATGTAAAAGCAGACTATAAACGCT<br>GC |
| BRCA1 | BRCA1_20 | 17 | 41243373 | 41243569 | ACACTGACGACATGGTTCTACAATGTGCTCCCCAAAAGCATAAAC | TACGGTAGCAGAGACTTGGTCTCAGTCTGAAAGCCAGGGAGTTG | 197 | 41 | ATGTGCTCCCCAAAAGCATAAACATTTAGCTCACTTCTATAAATAGACTG<br>GGGCAAACACAAAAACCTGGTTCCAATACCTAAGTTTGAATCCATGCTTT<br>GCTCTTCTTGATTATTTTCTTCCAAGCCCGTTCCTCTTTCTTCATCATCTG<br>AAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTTCAGACTG |

Assays designed by relax mode and have no off-target hits

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| BRCA1 | BRCA1_21 | 17 | 41243485 | 41243674 | ACACTGACGACATGGTTCTACATATTTTCTTCCAAGCCCGTTCCT | TACGGTAGCAGAGACTTGGTCTTCTGCTAGCTTGTTTTCTTCACA | 190 | 43 | TATTTTCTTCCAAGCCCGTTCCTCTTTCTTCATCATCTGAAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTTCAGACTGATGCCTCATTTGTTTGGAAGAACCAATCAAGAAAGGATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAATTCACTGCACTGTGAAGAAAACAAGCTAGCAGA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_22 | 17 | 41243604 | 41243793 | ACACTGACGACATGGTTCTACAGGATCCTGGGTGTTTGTATTTTGC | TACGGTAGCAGAGACTTGGTCTTGTCTAAGAACACAGAGGAGAATTTA | 190 | 39 | GGATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAATTCACTGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTTCCTCACTAAGGTGATGTTCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTGTTCTTAGACA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_23 | 17 | 41243699 | 41243897 | ACACTGACGACATGGTTCTACAATGTTCCTGAGATGCCTTTGCC | TACGGTAGCAGAGACTTGGTCTTAGTGAGGATGAAGAGCTTCCCT | 199 | 40 | ATGTTCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCATTTAAGCTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTGTTCTTAGACAGACACTCGGTAGCAACGGTGCTATGCCTAGTAGACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCATCCTCACTA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_24 | 17 | 41243852 | 41244044 | ACACTGACGACATGGTTCTACAACCAAATAACAAGTGTTGGAAGC | TACGGTAGCAGAGACTTGGTCTTGACATTAAGGAAAGTTCTGCTGTT | 193 | 45 | ACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_25 | 17 | 41243949 | 41244145 | ACACTGACGACATGGTTCTACATGAGCCAAATGTGTATGGGTGAA | TACGGTAGCAGAGACTTGGTCTCAGCCTATGGGAAGTAGTCATGC | 197 | 43 | TGAGCCAAATGTGTATGGGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCATTTTCAGCAAAACTAGTATCTTCCTTTATTTCACCATCATCTAACAGGTCATCAGGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCCGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCATTTTCAGCAAAA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_26 | 17 | 41244007 | 41244197 | ACACTGACGACATGGTTCTACACGCTTTTGCTAAAAACAGCAGAAC | TACGGTAGCAGAGACTTGGTCTTCAGACTGTTAATACAGATTTCTCTCCA | 191 | 37 | CTAGTATCTTCCTTTATTTCACCATCATCTAACAGGTCATCAGGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCTGTATTAACAGTCTGA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_27 | 17 | 41244115 | 41244295 | ACACTGACGACATGGTTCTACACCTGAGATGCATGACTACTTCCC | TACGGTAGCAGAGACTTGGTCTAGATTAGGGGTTTTGCAACCTGA | 181 | 36 | CCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCTGTATTAACAGTCTGAACTACTTCTTCATATTCTTGCTTTTTTATTTCAGGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCTAGACCTCAGGTTGCAAAACCCCTAATCT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_28 | 17 | 41244171 | 41244361 | ACACTGACGACATGGTTCTACAGGAGAGAAATCTGTATTAACAGTCTGAAC | TACGGTAGCAGAGACTTGGTCTTCCAGTGATGAAAACATTCAAGCA | 191 | 37 | GGAGAGAAATCTGTATTAACAGTCTGAACTACTTCTTCATATTCTTGCTTTTTTATTTCAGGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTTCATCactgga | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_29 | 17 | 41244266 | 41244448 | ACACTGACGACATGGTTCTACAATAGACCTCAGGTTGCAAAACCC | TACGGTAGCAGAGACTTGGTCTAATGTTTTTAAAGAAGCCAGCTCA | 183 | 38 | ATAGACCTCAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTTCATCactggaacctatttcattaatactggagcccacttcattagtactggaacctacttcattaataTTGCTTGAGCTGGCTTCTTTTAAAAACATT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_30 | 17 | 41244375 | 41244557 | ACACTGACGACATGGTTCTACAATACTGGAGCCCACTTCATTAGT | TACGGTAGCAGAGACTTGGTCTTCTGCTAGAGGAAAACTTTGAGGA | 183 | 37 | atactggagcccacttcattagtactggaacctacttcattaataTTGCTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTATTACGGCTAATTGTGCTCACTGTACTTGGAATGTTCTCATTTCCCATTTCTCTTTCAGGTGACATTGAATGTTCCTCAAAGTTTTCCTCTAGCAGA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_31 | 17 | 41244473 | 41244671 | ACACTGACGACATGGTTCTACATGTGCTCACTGTACTTGGAATGT | TACGGTAGCAGAGACTTGGTCTAGGCAACGAAACTGGACTCATTA | 199 | 36 | TGTGCTCACTGTACTTGGAATGTTCTCATTTCCCATTTCTCTTTCAGGTGACATTGAATGTTCCTCAAAGTTTTAACAAATGACTTGATGGGAAAAAGTGGTGGTATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAATGAGTCCAGTTTCGTTGCCT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_32 | 17 | 41244586 | 41244763 | ACACTGACGACATGGTTCTACAACTTGATGGGAAAAAGTGGTGGT | TACGGTAGCAGAGACTTGGTCTTTTCCTGTGGTTGGTCAGAAAGA | 178 | 39 | ACTTGATGGGAAAAAGTGGTGGTATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAATGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAAACCTAGAGCCTCCTTTGATACTACATTTGGCATTATCAACTGGCTTATCTTTCTGACCAACCACAGGAAA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_33 | 17 | 41244648 | 41244841 | ACACTGACGACATGGTTCTACAGTAATGAGTCCAGTTTCGTTGCC | TACGGTAGCAGAGACTTGGTCTTGTGAACAAAAGGAAGAAAATCAAGGA | 194 | 40 | GTAATGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAAACCTAGAGCCTCCTTTGATACTACATTTGGCATTATCAACTGGCTTATCTTTCTGACCAACCACAGGAAAGCCTGCAGTGATATTAACTGTCTGTACAGGCTTGATATTAGACTCATTCTTTCCTTGATTTTCTTCCTTTTGTTCACA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_34 | 17 | 41244742 | 41244940 | ACACTGACGACATGGTTCTACACTTTCTGACCAACCACAGGAAAG | TACGGTAGCAGAGACTTGGTCTGCTCCGTTTTCAAATCCAGGAAA | 199 | 41 | CTTTCTGACCAACCACAGGAAAGCCTGCAGTGATATTAACTGTCTGTACAGGCTTGATATTAGACTCATTCTTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGACTTTTGGACTTTGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCATTTCCTGGATTTGAAAACGGAGC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_35 | 17 | 41244864 | 41245040 | ACACTGACGACATGGTTCTACATGTTTCTTTAAGGACCCAGAGTG | TACGGTAGCAGAGACTTGGTCTAGTTAACCACAGTCGGGAAACAA | 177 | 42 | TGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCATTTCCTGGATTTGAAAACGGAGCTTGAATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCATTTCTATGCTTGTTTCCCGACTGTGGTTAACT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_36 | 17 | 41244947 | 41245144 | ACACTGACGACATGGTTCTACACTGGCGCTTTGAAACCTTGAAT | TACGGTAGCAGAGACTTGGTCTGTGAGTCAGTGTGCAGCATTTG | 198 | 40 | CTGGCGCTTTGAAACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCATTTCTATGCTTGTTTCCCGACTGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGTGTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGACTCAC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_37 | 17 | 41245044 | 41245232 | ACACTGACGACATGGTTCTACATGTCCCAATGGATACTTAAAGCC | TACGGTAGCAGAGACTTGGTCTACCTGGTACTGATTATGGCACTC | 189 | 41 | TGTCCCAATGGATACTTAAAGCCTTCTGTGTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGACTCACACATTTATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_38 | 17 | 41245154 | 41245339 | ACACTGACGACATGGTTCTACATGGTTCTGTTTTTGCCTTCCCTA | TACGGTAGCAGAGACTTGGTCTACAGTTAAAGTGTCTAATAATGCTGAAGA | 186 | 40 | TGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTCAGTTTGCAAAACCCTTTCTCCACTTAACATGAGATCTTTGGGGTCTTCAGCATTATTAGACACTTTAACTGT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_39 | 17 | 41245246 | 41245433 | ACACTGACGACATGGTTCTACATGCTACTCTCTACAGATCTTTCAGTT | TACGGTAGCAGAGACTTGGTCTACCTGGTTCTTTTACTAAGTGTTCAAA | 188 | 36 | TGCTACTCTCTACAGATCTTTCAGTTTGCAAAACCCTTTCTCCACTTAACATGAGATCTTTGGGGTCTTCAGCATTATTAGACACTTTAACTGTTTCTAGTT | Assays designed by relax mode and have no off-target hits |

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| | | | | | | | | | TCTCTTCTTTTTCTTCTCTTGGAAGGCTAGGATTGACAAATTCTTTAAGTT CACTGGTATTTGAACACTTAGTAAAAGAACCAGGT | |
| BRCA1 | BRCA1_40 | 17 | 41245357 | 41245539 | ACACTGACGACATGGTTCTA CATTTCTTCTCTTGGAAGGC TAGGA | TACGGTAGCAGAGACTTGGTCTA AGGTAAAGAACCTGCAACTGGA | 183 | 39 | TTTCTTCTCTTGGAAGGCTAGGATTGACAAATTCTTTAAGTTCACTGGTAT TTGAACACTTAGTAAAAGAACCAGGTGCATTTGTTAACTTCAGCTCTGGG AAAGTATCGCTGTCATGTCTTTTACTTGTCTGTTCATTTGGCTTGTTACTC TTCTTGGCTCCAGTTGCAGGTTCTTTACCTT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_41 | 17 | 41245455 | 41245653 | ACACTGACGACATGGTTCTA CAGGGAAAGTATCGCTGTCA TGTCT | TACGGTAGCAGAGACTTGGTCTG CCCACCTAATTGTACTGAATTGC | 199 | 41 | GGGAAAGTATCGCTGTCATGTCTTTTACTTGTCTGTTCATTTGGCTTGTT ACTCTTCTTGGCTCCAGTTGCAGGTTCTTTACCTTCCATGAGTTGTAGGT TTCTGCTGTGCCTGACTGGCATTTGGTTGTACTTTTTTTTCTTTATCTCTT CACTGCTAGAACAACTATCAATTTGCAATTCAGTACAATTAGGTGGGC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_42 | 17 | 41245543 | 41245737 | ACACTGACGACATGGTTCTA CATGAGTTGTAGGTTTCTGC TGTGC | TACGGTAGCAGAGACTTGGTCTA AGCACCTAAAAAGAATAGGCTGA | 195 | 39 | TGAGTTGTAGGTTTCTGCTGTGCCTGACTGGCATTTGGTTGTACTTTTTT TTCTTTATCTCTTCACTGCTAGAACAACTATCAATTTGCAATTCAGTACAA TTAGGTGGGCTTAGATTTCTACTGACTACTAGTTCAAGCGCATGAATATG CCTGGTAGAAGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_43 | 17 | 41245646 | 41245835 | ACACTGACGACATGGTTCTA CAAGGTGGGCTTAGATTTCT ACTGAC | TACGGTAGCAGAGACTTGGTCTA GAATCACTCGAAAAAGAATCTGC | 190 | 38 | AGGTGGGCTTAGATTTCTACTGACTACTAGTTCAAGCGCATGAATATGCC TGGTAGAAGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTTTGAATTG TGGATATTTAATTCGAGTTCCATATTGCTTATACTGCTGCTTATAGGTTCA GCTTTCGTTTTGAAAGCAGATTCTTTTTCGAGTGATTCT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_44 | 17 | 41245703 | 41245894 | ACACTGACGACATGGTTCTA CAAGACTTCCTCCTCAGCCT ATTCT | TACGGTAGCAGAGACTTGGTCTG GTCATGAGAATAAAACAAAAGGT GATTCT | 192 | 35 | AGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTATAGGTTCAGCTTTCGT TTTGAAAGCAGATTCTTTTTCGAGTGATTCTATTGGGTTAGGATTTTTCTC ATTCTGAATAGAATCACCTTTTGTTTTATTCTCATGACC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_45 | 17 | 41245824 | 41245994 | ACACTGACGACATGGTTCTA CATCGAGTGATTCTATTGGG TTAGGA | TACGGTAGCAGAGACTTGGTCTC AAGAAAGCAGATTTGGCAGTTCA | 171 | 36 | TCGAGTGATTCTATTGGGTTAGGATTTTTCTCATTCTGAATAGAATCACCT TTTGTTTTATTCTCATGACCACTATTAGTAATATTCATCACTTGACCATTCT GCTCCGTTTGGTTAGTTCCCTGATTTATCATTTCAGGAGTCTTTTGAACT GCCAAATCTGCTTTCTTG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_46 | 17 | 41245929 | 41246123 | ACACTGACGACATGGTTCTA CATCCGTTTGGTTAGTTCCC TGATTT | TACGGTAGCAGAGACTTGGTCTC CATGTAACTGAAAATCTAATTATA GGAGCA | 195 | 38 | TCCGTTTGGTTAGTTCCCTGATTTATCATTTCAGGAGTCTTTTGAACTGC CAAATCTGCTTTCTTGATAAAATCCTCAGGATGAAGGCCTGATGTAGGTC TCCTTTTACGCTTTAATTTATTTGTGAGGGGACGCTCTTGTATTATCTGTG GCTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_47 | 17 | 41246014 | 41246212 | ACACTGACGACATGGTTCTA CAGGCCTGATGTAGGTCTCC TTTTA | TACGGTAGCAGAGACTTGGTCTA GAGTTCACTCCAAATCAGTAGAG | 199 | 39 | GGCCTGATGTAGGTCTCCTTTTACGCTTTAATTTATTTGTGAGGGGACGC TCTTGTATTATCTGTGGCTCAGTAACAAATGCTCCTATAATTAGATTTTCA GTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCC CAAATATTTTGTCTTCAATATTACTCTCTACTGATTTGGAGTGAACTCT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_48 | 17 | 41246138 | 41246324 | ACACTGACGACATGGTTCTA CAGCTTGCCTTCTTCCGATA GGT | TACGGTAGCAGAGACTTGGTCTA GTAGCTGATGTATTGGACGTTCT | 187 | 37 | GCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACT CTCTACTGATTTGGAGTGAACTCTTTCACTTTTACATATTAAAGCCTCATG AGGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCAT CTACCTCATTTAGAACGTCCAATACATCAGCTACT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_49 | 17 | 41246190 | 41246388 | ACACTGACGACATGGTTCTA CATCTACTGATTTGGAGTGA ACTCTTT | TACGGTAGCAGAGACTTGGTCTC CAGAAGTGATGAACTGTTAGGT | 199 | 39 | TCTACTGATTTGGAGTGAACTCTTTCACTTTTACATATTAAAGCCTCATGA GGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCATC TACCTCATTTAGAACGTCCAATACATCAGCTACTTTGGCATTTGATTCAG ACTCCCCATCATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_50 | 17 | 41246313 | 41246488 | ACACTGACGACATGGTTCTA CAACATCAGCTACTTTGGCA TTTGA | TACGGTAGCAGAGACTTGGTCTA ATAAGCAGAAACTGCCATGCTC | 176 | 40 | ACATCAGCTACTTTGGCATTTGATTCAGACTCCCCATCATGTGAGTCATC AGAACCTAACAGTTCATCACTTCTGGAAAACCACTCATTAACTTTCTGAA TGCTGCTATTTAGTGTTATCCAAGGAACATCTTCAGTATCTCTAGGATTC TCTGAGCATGGCAGTTTCTGCTTATT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_51 | 17 | 41246413 | 41246606 | ACACTGACGACATGGTTCTA CATGCTGCTATTTAGTGTTAT CCAAGG | TACGGTAGCAGAGACTTGGTCTA AGGAGCCAACATAACAGATGGG | 194 | 43 | TGCTGCTATTTAGTGTTATCCAAGGAACATCTTCAGTATCTCTAGGATTC TCTGAGCATGGCAGTTTCTGCTTATTCCATTCTTTTCTCTCACACAGGGG ATCAGCATTCAGATCTACCTTTTTTTCTGTGCTGGGAGTCCGCCTATCAT TACATGTTTCCTTACTTCCAGCCCATCTGTTATGTTGGCTCCTT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_52 | 17 | 41246501 | 41246699 | ACACTGACGACATGGTTCTA CACTCACACAGGGGATCAGC ATTC | TACGGTAGCAGAGACTTGGTCTA CAGCATGAGAACAGCAGTTTATT | 199 | 42 | CTCACACAGGGGATCAGCATTCAGATCTACCTTTTTTTCTGTGCTGGGA GTCCGCCTATCATTACATGTTTCCTTACTTCCAGCCCATCTGTTATGTTG GCTCCTTGCTAAGCCAGGCTGTTTGCTTTTATTACAGAATTCAGCCTTTT CTACATTCATTCTGTCTTTAGTGAGTAATAAACTGCTGTTCTCATGCTGT | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_53 | 17 | 41246584 | 41246781 | ACACTGACGACATGGTTCTA CACCCATCTGTTATGTTGGC TCCTT | TACGGTAGCAGAGACTTGGTCTG GCATCCAGAAAAGTATCAGGGTA | 198 | 42 | CCCATCTGTTATGTTGGCTCCTTGCTAAGCCAGGCTGTTTGCTTTTATTA CAGAATTCAGCCTTTTCTACATTCATTCTGTCTTTAGTGAGTAATAAACTG CTGTTCTCATGCTGTAATGAGCTGGCATGAGTATTTGTGCCACATGGCT CCACATGCAAGTTTGAAACAGAACTACCCTGATACTTTTCTGGATGCC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_54 | 17 | 41246695 | 41246882 | ACACTGACGACATGGTTCTA CAGCTGTAATGAGCTGGCAT GAGTA | TACGGTAGCAGAGACTTGGTCTT TCAGCTGCTTGTGAATTTTCTG | 188 | 43 | GCTGTAATGAGCTGGCATGAGTATTTGTGCCACATGGCTCCACATGCAA GTTTGAAACAGAACTACCCTGATACTTTTCTGGATGCCTCTCAGCTGCAC GCTTCTCAGTGGTGTTCAAATCATTATTACTGGGTTGATGATGTTCAGTA TTTGTTACATCCGTCTCAGAAAATTCACAAGCAGCTGAA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_55 | 17 | 41246761 | 41246959 | ACACTGACGACATGGTTCTA CACCTGATACTTTTCTGGAT GCCTCT | TACGGTAGCAGAGACTTGGTCTC CACCTCCAAGGTGTATGAAGTA | 199 | 37 | CCTGATACTTTTCTGGATGCCTCTCAGCTGCACGCTTCTCAGTGGTGTTC AAATCATTATTACTGGGTTGATGATGTTCAGTATTTGTTACATCCGTCTCA GAAAATTCACAAGCAGCTGAAAATATACAAAAATAACAAGGTACTCAAAA ACTGAATTGTCATTAAAAAAATACATACTTCATACACCTTGGAGGTGG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_56 | 17 | 41247808 | 41248006 | ACACTGACGACATGGTTCTA CATGTATCTACCCACTCTCTT TTCAGT | TACGGTAGCAGAGACTTGGTCTG GTCATTTGACAGTTCTGCATAC | 199 | 40 | TGTATCTACCCACTCTCTTTTCAGTGCCTGTTAAGTTGGCAAACTTTGCC ATTACCCTTTTTTGCAGAATCCAAACTGATTTCATCCCTGGTTCCTTGAG GGGTGATTTGTAACAATTCTTGATCTCCCACACTATAGGGAAAAGACAGA GTCCTAATAAGAAACACTAGTTACATGTATGCAGAACTGTCAAATGACC acaaactgcacatacatccctgaacctaaaataaaagttaaaaTATTTTTAAAAAGAGAGAA | |
| BRCA1 | BRCA1_57 | 17 | 41249130 | 41249324 | ACACTGACGACATGGTTCTA CAACAAACTGCACATACATC CCTGA | TACGGTAGCAGAGACTTGGTCTT GGGGGGAAATTTTTTAGGATCTG | 195 | 32 | ACATCAATCCTTAATATTAACTAAATAGGAAAATACCAGCTTCATAGACAA AGGTTCTCTTTGACTCACCTGCAATAAGTTGCCTTATTAACGGTATCTTC AGAAGAATCAGATCCTAAAAAATTTCCCCCCA | Assays designed by relax mode and have no off-target hits |

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| BRCA1 | BRCA1_58 | 17 | 41249255 | 41249439 | ACACTGACGACATGGTTCTACCAACTCACCTGCAATAAGTTGCCTT | TACGGTAGCAGAGACTTGGTCTGCATTGTACCTGCCACAGTAGAT | 185 | 31 | ACTCACCTGCAATAAGTTGCCTTATTAACGGTATCTTCAGAAGAATCAGATCCTAAAAAATTTCCCCCCAAAAAATAAATCAATAAAAGTTTTCTTAATTAAAAGGGTTAAAAAAATGTACTTGTTGAAAAACAGATattcaactagaaatatttactgagcatctactgtggcaggtacaatgc | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_59 | 17 | 41251674 | 41251855 | ACACTGACGACATGGTTCTACAATTCACTTCCCAAAGCTGCCTAC | TACGGTAGCAGAGACTTGGTCTGTGAGAACTCTGAGGACAAAGCA | 182 | 37 | ATTCACTTCCCAAAGCTGCCTACCACAAATACAAATTATGACCAAGATTTTTGGCAAAACTATAAGATAAGGAATCCAGCAATTATTATTAAATACTTAAAAAACCTGAGACCCTTACCCAATTCAATGTAGACAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCAC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_60 | 17 | 41251773 | 41251963 | ACACTGACGACATGGTTCTACAAAAAACCTGAGACCCTTACCCAA | TACGGTAGCAGAGACTTGGTCTCTCTTCAGGAGGAAAAGCACAGA | 191 | 45 | AAAAACCTGAGACCCTTACCCAATTCAATGTAGACAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCACAGTTCCAAGGTTAGAGAGTTGGACACTGAGACTGGTTTCCTGCTAAACAGTATGGTAAAGAACAGTCAAGCAATTGTTGGCCAGTTCTGTGCTTTTCCTCCTGAAGAG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_61 | 17 | 41256105 | 41256293 | ACACTGACGACATGGTTCTACAAGAAGAAGAAGAAGAAAAACAAATGG | TACGGTAGCAGAGACTTGGTCTCCTTGTATTTTACAGATGCAAACAGC | 189 | 35 | agaagaagaagaagaagaaAACAAATGGTTTTACCAAGGAAGGATTTTCGGGTTCACTCTGTAGAAGTCTTTTGGCACGGTTTCTGTAGCCCATACTTTGGATGATAGAAACTTCAAAATTATAGCTGTTTGCATCTGTAAAATACAAGG | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_62 | 17 | 41256170 | 41256368 | ACACTGACGACATGGTTCTACAAGTCTTTTGGCACGGTTTCTGTA | TACGGTAGCAGAGACTTGGTCTGCATACATAGGGTTTCTCTTGGT | 199 | 33 | AGTCTTTTGGCACGGTTTCTGTAGCCCATACTTTGGATGATAGAAACTTCATCTTTTAGATGTTCAGGAGAGTTATTTTCCTTTTTTGCAAAATTATAGCTGTTTGCATCTGTAAAATACAAGGGAAAACATTATGTTTGCAGTTAGAGAAAAATGTATGAATTATAATCAAAGAAACCAAGAGAAACCCTATGTATGC | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_63 | 17 | 41256828 | 41257012 | ACACTGACGACATGGTTCTACATTCCTGAGTTTTCATGGACAGCA | TACGGTAGCAGAGACTTGGTCTTCACTTGCTGAGTGTGTTTCTCA | 185 | 38 | TTCCTGAGTTTTCATGGACAGCACTTGAGTGTCATTCTTGGGATATTCAACACTTACACTCCAAACCTGTGTCAAGCTGAAAAGCACAAATGATTTTCAATAGCTCTTCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTGAAATTAAATTGTTTGAGAAACACACTCAGCAAGTGA | Assays designed by relax mode and have no off-target hits |
| BRCA1 | BRCA1_64 | 17 | 41258420 | 41258615 | ACACTGACGACATGGTTCTACAACTTTTTCCTACTGTGGTTGCTT | TACGGTAGCAGAGACTTGGTCTTTTTGAGTATTCTTTCTACAAAAGGAAGTAAAT | 196 | 31 | ACTTTTTCCTACTGTGGTTGCTTCCAACCTAGCATCATTACCAAATTATATACCTTTTGGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTTCTGGTTGAGAAGTTTCAGCATGCAAAATCTATAAATTATAAAGAAAGAAAGAACAATTTAATTTACTTCCTTTTGTAGAAAGAATACTCAAAA | |
| BRCA1 | BRCA1_65 | 17 | 41267715 | 41267905 | ACACTGACGACATGGTTCTACATGGAGCCACATAACACATTCAAA | TACGGTAGCAGAGACTTGGTCTACTCAGTCATAACAGCTCAAAGT | 191 | 37 | TGGAGCCACATAACACATTCAAACTTACTTGCAAAATATGTGGTCACACTTTGTGGAGACAGGTTCCTTGATCAACTCCAGACTAGCAGGGTAGGGGGGGAGAAAAAGAAAATAAATGAGGCTCaataatttatttaaaaataaaGCTATTCTTAGTGAATAAGTTCAACTTTGAGCTGTTATGACTGAGT | |
| BRCA1 | BRCA1_Intron_2__region_1__1 | 17 | 41271145 | 41271333 | ACACTGACGACATGGTTCTACATGTGACAAGAATGTGGTTTTTTCCT | TACGGTAGCAGAGACTTGGTCTTCCACAAGCTTTTCTTGTGATCC | 189 | 42 | TGTGACAAGAATGTGGTTTTTTCCTTAAATATTTAACTTTTTAGAAAAGGATCACAAGggccaggtgcggtggctcacgctgtaatcccagcattttgggaggccaaggcgggccagcctgggtgacagagaatccatctcaaaaaaagaaaaaaaaaaaagaaaaGGATCACAAGAAAAGCTTGTGGA | |
| BRCA1 | BRCA1_Intron_2__region_1__2 | 17 | 41271314 | 41271508 | ACACTGACGACATGGTTCTACATCACAAGAAAAGCTTGTGGACAG | TACGGTAGCAGAGACTTGGTCTGAAACAGGTTCAGGTAGAGTGGT | 195 | 42 | TCACAAGAAAAGCTTGTGGACAGTAACCTTATTGTGAAGGGTTGTAATACAACTCTTGTAATCATGGGGTTTTTGACATAGCACAGGgcagtgaaaagaaaaacaatgaactaagtcaggaggctgggtttctactaccagttgtgtatataagcagagccaccttgggctaaccactctacctgaacctgtttc | One primer sits in the repeat region |
| BRCA1 | BRCA1_Intron_2__region_1__3 | 17 | 41271383 | 41271556 | ACACTGACGACATGGTTCTACATTTTTGACATAGCACAGGGCAGT | TACGGTAGCAGAGACTTGGTCTATTCTTGCAATAGCCCAAGGAGT | 174 | 45 | TTTTTGACATAGCACAGGgcagtgaaaagaaaaacaatgaactaagtcaggaggctgggtttctactaccagttgtgtatataagcagagccaccttgggctaaccactctacctgaacctgtttccttctcttgccattcaccctgccagactccttgggctattgcaagaata | Two primers sits in the repeat region |
| BRCA1 | BRCA1_Intron_2__region_1__4 | 17 | 41271482 | 41271675 | ACACTGACGACATGGTTCTACAGCTAACCACTCTACCTGAACCTG | TACGGTAGCAGAGACTTGGTCTAAAGTCACATTTGGTCCCAGTAA | 194 | 41 | gctaaccactctacctgaacctgtttccttctcttgccattcaccctgccagactccttgggctattgcaagaataaaattaaatgctacttgggaaaatgcttcacaacctgagatgacttgggaaaaatgcttcacaacctgagataacttgTACCAACATTGGTATTATTACTGGGACCAAATGTGACTTT | One primer sits in the repeat region |
| BRCA1 | BRCA1_Intron_2__region_1__5 | 17 | 41271534 | 41271710 | ACACTGACGACATGGTTCTACAACTCCTTGGGCTATTGCAAGAAT | TACGGTAGCAGAGACTTGGTCTTCAGAGTTTTCTTTGTCAAGGTTGTT | 177 | 36 | actccttgggctattgcaagaataaaattaaatgctacttgggaaaatgcttcacaacctgagatgacttgggaaaaatgcttcacaacctgagataacttgTACCAACATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCCATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCTTGACAAAGAAAACTCTGATTGGTTACTAAATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACT | One primer sits in the repeat region |
| BRCA1 | BRCA1_Intron_2__region_1__6 | 17 | 41271642 | 41271822 | ACACTGACGACATGGTTCTACACATTGGTATTATTACTGGGACCAAATGT | TACGGTAGCAGAGACTTGGTCTAGTCAGTGGTGAGAATGAAAGCC | 181 | 33 | CATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCTTGACAAAGAAAACTCTGATTGGTTACTAAATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACT | |
| BRCA1 | BRCA1_Intron_2__region_1__7 | 17 | 41271721 | 41271916 | ACACTGACGACATGGTTCTACAAATCCCTATTTCTGAGATAAGCTACAT | TACGGTAGCAGAGACTTGGTCTTCGGAGTTTTCATCTGTTCAAAGT | 196 | 31 | AATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGA | |
| BRCA1 | BRCA1_Intron_2__region_1__8 | 17 | 41271811 | 41272000 | ACACTGACGACATGGTTCTACATCACCACTGACTCAATTCTGAAAC | TACGGTAGCAGAGACTTGGTCTTCAGGACCTAGAAGGGGAACATT | 190 | 31 | TCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGATATGTAAAAAGGTAATGAATGTTGAAGGAAGACTGTGAAAAGGGAAAAGAAAAAAAATTAAAATGTTCCCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGA | |
| BRCA1 | BRCA1_Intron_2__region_1__9 | 17 | 41271942 | 41272115 | ACACTGACGACATGGTTCTACAAGGAAGACTGTGAAAAGGGAAAAGAA | TACGGTAGCAGAGACTTGGTCTTCACTTATCCGTATTGGAAGCTCA | 174 | 31 | TCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGATATGTAAAAAGGTAATGAATGTTGAAGGAAGACTGTGAAAAGGGAAAAGAAAAAAAATTAAAATGTTCCCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGA | |
| BRCA1 | BRCA1_Intron_2__region_1__10 | 17 | 41271985 | 41272159 | ACACTGACGACATGGTTCTACACCCTTCTAGGTCCTGATGAGAGTA | TACGGTAGCAGAGACTTGGTCTGGTGGGTTGTTGTTTTTCAACCT | 175 | 35 | CCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGACTGGAAAAAGCAGCTAGGTTTAGGTTGAAAAACAACAACCCACC | Multiple hits |
| BRCA1 | BRCA1_Intron_2__region_2__1 | 17 | 41275655 | 41275814 | ACACTGACGACATGGTTCTACAGCCCTCGGCCTCATCCAT | TACGGTAGCAGAGACTTGGTCTAATCCTGTGGTCCGGGAAAGAC | 160 | 46 | gccctcggccTCATCCATGATTTTATTTTGCCATTTCAAGTGATGGAGCTTGTTTTAGAGCTGGAAGAAAAGCCAAAATGCCAGTTAATCTAAACTAGATTCCTGCCCCAGTGCAGAACCAATCAAGACAGAGTCCCTGTCTTTCCCGGACCACAGGATT | One primer sits in the repeat region |

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| BRCA1 | BRCA1_Intron_2__region_2__3 | 17 | 41275694 | 41275869 | ACACTGACGACATGGTTCTACAGTGATGGAGCTTGTTTTAGAGCTG | TACGGTAGCAGAGACTTGGTCTTGATTCCTTGTTCTCCATCCACT | 176 | 47 | GTGATGGAGCTTGTTTTAGAGCTGGAAGAAAAGCCAAAATGCCAGTTAATCTAAACTAGATTCCTGCCCCAGTGCAGAACCAATCAAGACAGAGTCCCTGTCTTTCCCGGACCACAGGATTTGTGTTGAAAAGGAGAGGAGTGGGAGAGGCAGAGTGGATGGAGAACAAGGAATCA |
| BRCA1 | BRCA1_Intron_2__region_2__4 | 17 | 41275796 | 41275973 | ACACTGACGACATGGTTCTACATTTCCCGGACCACAGGATTTG | TACGGTAGCAGAGACTTGGTCTACAGAATTGACCTTACATACTAGGGG | 178 | 38 | TTTCCCGGACCACAGGATTTGTGTTGAAAAGGAGAGGAGTGGGAGAGGCAGAGTGGATGGAGAACAAGGAATCATTTTCTATATTTTTAAAGTTCTTCAGTTAAGAAAATCAGCAATTACAATAGCCTAATCTTACTAGACATGTCTTTTCTTCCCTAGTATGTAAGGTCAATTCTGT |
| BRCA1 | BRCA1_Intron_2__region_2__5 | 17 | 41275844 | 41276026 | ACACTGACGACATGGTTCTACACAGAGTGGATGGAGAACAAGGAA | TACGGTAGCAGAGACTTGGTCTAGCACAAGAGTGTATTAATTTGGGA | 183 | 33 | CAGAGTGGATGGAGAACAAGGAATCATTTTCTATATTTTTAAAGTTCTTCAGTTAAGAAAATCAGCAATTACAATAGCCTAATCTTACTAGACATGTCTTTTCTTCCCTAGTATGTAAGGTCAATTCTGTTCATTTGCATAGGAGATAATCATAGGAATCCCAAATTAATACACTCTTGTGCT |
| BRCA1 | BRCA1_66 | 17 | 41275974 | 41276147 | ACACTGACGACATGGTTCTACATCATTTGCATAGGAGATAATCATAGGAA | TACGGTAGCAGAGACTTGGTCTTCTAATGTGTTAAAGTTCATTGGAACAG | 174 | 35 | TCATTTGCATAGGAGATAATCATAGGAATCCCAAATTAATACACTCTTGTGCTGACTTACCAGATGGGACACTCTAAGATTTTCTGCATAGCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAATCCATTTCTTTCTGTTCCAATGAACTTTAACACATTAGA |
| BRCA1 | BRCA1_5_UTR__exon_1B__1 | 17 | 41277107 | 41277305 | ACACTGACGACATGGTTCTACACTTCCCTCGCGACCTACAAAAC | TACGGTAGCAGAGACTTGGTCTCCTCTGCTCTGGGTAAAGGTAGT | 199 | 60 | CTTCCCTCGCGACCTACAAACTGCCCCCCTCCCCAGGGTTCACAACGCCTTACGCCTCTCAGGTTCCGCCCCTACCCCCCGTCAAAGAATACCCATCTGTCAGCTTCGGAAATCCACTCTCCCACGCCAGTACCCCAGAGCATCACTTGGGCCCCCTGTCCCTTTCCCGGGACTCTACTACCTTTACCCAGAGCAGAGG |
| BRCA1 | BRCA1_prom1AextF_1 | 17 | 41277234 | 41277419 | ACACTGACGACATGGTTCTACACAGTACCCCAGAGCATCACTT | TACGGTAGCAGAGACTTGGTCTACAGATAAATTAAAACTGCGACTGC | 186 | 59 | CAGTACCCCAGAGCATCACTTGGGCCCCCTGTCCCTTTCCCGGGACTCTACTACCTTTACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAGGGGCCCAGTTATCTGAGAAACCCCACAGCCTGTCCCCCGTCCAGGAAGTCTCAGCGAGCTCACGCCGCGCAGTCGCAGTTTTAATTTATCTGT |
| BRCA1 | BRCA1_5_UTR__exon_1A__2 | 17 | 41277330 | 41277526 | ACACTGACGACATGGTTCTACACCCAGTTATCTGAGAAACCCCAC | TACGGTAGCAGAGACTTGGTCTCTTTCTGTCCCTCCCATCCTCT | 197 | 54 | CCCAGTTATCTGAGAAACCCCACAGCCTGTCCCCCGTCCAGGAAGTCTCAGCGAGCTCACGCCGCGCAGTCGCAGTTTTAATTTATCTGTAATTCCCGCGCTTTTCCGTTGCCACGGAAACCAAGGGGCTACCGCTAAGCAGCAGCCTCTCAGAATACGAAATCAAGGTACAATCAGAGGATGGGAGGGACAGAAAG |
| BRCA1 | BRCA1_prom1AextF_3 | 17 | 41277442 | 41277637 | ACACTGACGACATGGTTCTACACACGGAAACCAAGGGGCTAC | TACGGTAGCAGAGACTTGGTCTAGGCACTTTATGGCAAACTCAGG | 196 | 53 | CACGGAAACCAAGGGGCTACCGCTAAGCAGCAGCCTCTCAGAATACGAAATCAAGGTACAATCAGAGGATGGGAGGGACAGAAAGAGCCAAGCGTCTCTCGGGGCTCTGGATTGGCCACCCAGTCTGCCCCCGGATGACGTAAAGGAAAGAGACGGAAGAGGAAGAATTCTACCTGAGTTTGCCATAAAGTGCCT |
| BRCA1 | BRCA1_prom1AextF_4 | 17 | 41277536 | 41277729 | ACACTGACGACATGGTTCTACATCTCTCGGGGCTCTGGATTG | TACGGTAGCAGAGACTTGGTCTACTGCTTTGGACAATAGGTAGCG | 194 | 51 | TCTCTCGGGGCTCTGGATTGGCCACCCAGTCTGCCCCCGGATGACGTAAAAGGAAAGAGACGGAAGAGGAAGAATTCTACCTGAGTTTGCCATAAAGTGCCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGGTCAGAATCGCTACCTATTGTCCAAAGCAGT |
| BRCA1 | BRCA1_Promoter_3 | 17 | 41277639 | 41277818 | ACACTGACGACATGGTTCTACACCCTCTAGCCTCTACTCTTCCAG | TACGGTAGCAGAGACTTGGTCTCCCCCCAACAATCCTTATTACTT | 180 | 48 | CCCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGGTCAGAATCGCTACCTATTGTCCAAAGCAGTCGTAAGAAGAGGTCCCAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATATAAGTAATAAGGATTGTTGGGGGG |
| BRCA1 | BRCA1_Promoter_4 | 17 | 41277726 | 41277921 | ACACTGACGACATGGTTCTACACAGTCGTAAGAAGAGGTCCCAAT | TACGGTAGCAGAGACTTGGTCTTGGTATTGGATGTTCCTCTCCAT | 196 | 46 | CAGTCGTAAGAAGAGGTCCCAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATATAAGTAATAAGGATTGTTGGGGGGGTGGAGGGGAAATAATTATTTCCAGCATGCGTTGCGGAATGAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCAATACCA |
| BRCA1 | BRCA1_Promoter_5 | 17 | 41277847 | 41278043 | ACACTGACGACATGGTTCTACACGTTGCGGAATGAAAGGTCTTC | TACGGTAGCAGAGACTTGGTCTAGGCCTAGTTTCTGCTTTCAAAAT | 197 | 46 | CGTTGCGGAATGAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCAATACCAGAGCGGGCACAATTCTCACGGAAATCCAGTGGATAGATTGGAGACCTGTGCGCGCTTGTACTTGTCAACAGTTATGGACTGGAGTGTTATGTTTTCGTATTTTGAAAGCAGAAACTAGGCCTGGAGAGGAACATCCAATACCAGAGCGGGCACAATTCTCACGGAAATCCA |
| BRCA1 | BRCA1_Promoter_6 | 17 | 41277901 | 41278096 | ACACTGACGACATGGTTCTACAGGAGAGGAACATCCAATACCAGAG | TACGGTAGCAGAGACTTGGTCTCTGGGGCTGGATGGGAATTG | 196 | 45 | GTGGATAGATTGGAGACCTGTGCGCGCTTGTACTTGTCAACAGTTATGGACTGGAGTGTTATGTTTTCGTATTTTGAAAGCAGAAACTAGGCCTTAAAAAGATACGTACAACTCTTTAGGGAGACTACAATTCCCATCCAGCCCCAGGAGTCTGGGGCAAGTAGTCTTGTAAGGTCAGTGGCCTGCGGGGACGCAGTGAGCGCCGAATTTGCCTGGGGCAGGG |
| BRCA1 | BRCA1_Promoter_7 | 17 | 41278016 | 41278210 | ACACTGACGACATGGTTCTACATCGTATTTTGAAAGCAGAAACTAGGC | TACGGTAGCAGAGACTTGGTCTGAACTACGAGTGCGCAGACA | 195 | 53 | TCGTATTTTGAAAGCAGAAACTAGGCCTTAAAAAGATACGTACAACTCTTTAGGGAGACTACAATTCCCATCCAGCCCCAGGAGTCTGGGGCAAGTAGCTGGGGCAGGGGAAATGCGCTCTGGCCCATGTCTGCGCACTCGTAGTTC |
| BRCA1 | BRCA1_Promoter_8 | 17 | 41278126 | 41278324 | ACACTGACGACATGGTTCTACAAGTGGCCTGCGGGGAC | TACGGTAGCAGAGACTTGGTCTTTACCACTTGTCCCTCAAAACGA | 199 | 59 | AGTGGCCTGCGGGGACGCAGTGAGCGCCGAATTTGCCTGGGGCAGGGGAAATGCGCTCTGGCCCATGTCTGCGCACTCGTAGTTCCACCCCTCAGCCCCAGTGTTTGTTATTTTTCGGGTTCAGCTTGCTTTTGCCCCGTCTCCGTCGACGCAATCGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGTGGTAA |
| BRCA1 | BRCA1_Promoter_9 | 17 | 41278254 | 41278449 | ACACTGACGACATGGTTCTACACTTTTGCCCCCGTCTCCGT | TACGGTAGCAGAGACTTGGTCTGAGGCGGCAATGCAAAGAC | 196 | 56 | CTTTTGCCCCGTCTCCGTCGACGCAATCGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGTGGTAAGAGCCAATCTTCTTGGCGAAAACGCGGAGAAACGGGACTAGTTACTGTCTTTGTCCGCCATGTTAGATTCACCCCACAGAGATAGCGGCAGAGCTGGCAGCGGACGGTCTTTGCATTGCCGCCTC |
| BRCA1 | BRCA1_Promoter_10 | 17 | 41278347 | 41278528 | ACACTGACGACATGGTTCTACACGCGGAGAAACGGGACTAGTTA | TACGGTAGCAGAGACTTGGTCTCTCCAAACCCTCTTAGTGTGACG | 182 | 59 | CGCGGAGAAACGGGACTAGTTACTGTCTTTGTCCGCCATGTTAGATTCACCCCACAGAGATAGCGGCAGAGCTGGCAGCGGACGGTCTTTGCATTGCCGCCTCCCCACAGGGGCGGGAAGCTGGTAAGGAAGCAGCCTGGGTTAGCTAGGGGTGGGGTCACGTCACACTAAGAGGGTTTGGAG |

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| BRCA1_3UTR_Combined | BRCA1_3UTR_Combined_14 | 17 | 41196714 | 41196888 | ACACTGACGACATGGTTCTACATCTTTGGAAACCGGTTCTTG | TACGGTAGCAGAGACTTGGTCTAGATCATACCACGGCACTCC | 175 | 35 | TCTTTGGAAACCGGTTCTTGAAAATCTTCTGCTGTTTTAGAACACATTCTTTAGAAATCTAGCAAATATATCTCAGACTTTTAGAAATCTCTTCTAGTTTCATTTTCCTTTTTTTTTTTTTTTTTTTTGAGCCACAGTCTCACTGTCACCCAGGCTGGAGTGCCGTGGTATGATCT |
| BRCA1_3UTR_Combined | BRCA1_3UTR_Combined_15 | 17 | 41197039 | 41197205 | ACACTGACGACATGGTTCTACATCGAACTCCTGACCTCCAGT | TACGGTAGCAGAGACTTGGTCTGTCCTTGGGCAGTTCTCAAA | 167 | 51 | TCGAACTCCTGACCTCCAGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGCCCAGGTTTCAAGTTTCCTTTTCATTTCTAATACCTGCCTCAGAATTTCCTCCCCAATGTTCCACTCCAACATTTGAGAACTGCCCAAGGAC |
| BRCA1_Intron_2__region_1_ | BRCA1_Intron_2__region_1__11 | 17 | 41271259 | 41271409 | ACACTGACGACATGGTTCTACACAGCCTGGGTGACAGAGAAT | TACGGTAGCAGAGACTTGGTCTTTTCACTGCCCTGTGCTATG | 151 | 38 | CAGCCTGGGTGACAGAGAATCCATCTCAAAAAAAGAAAAAAAAAAAAGAAAAGGATCACAAGAAAAGCTTGTGGACAGTAACCTTATTGTGAAGGGTTGTAATACAACTCTTGTAATCATGGGGTTTTTGACATAGCACAGGGCAGTGAAA |
| BRCA1_Intron_2__region_2_ | BRCA1_Intron_2__region_2__7 | 17 | 41275415 | 41275564 | ACACTGACGACATGGTTCTACATGGAGTTCAGTGGTGCCATA | TACGGTAGCAGAGACTTGGTCTTGAAACCCCCTCTCCACTAA | 150 | 50 | TGGAGTTCAGTGGTGCCATATTGGCTCACAGCAACATCTGCCTCCTGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACTACGCCCAGCTAATTTTTGTATTTTTAGTGGAGAGGGGGTTTCA |
| BRCA1_Intron_2__region_2_ | BRCA1_Intron_2__region_2__8 | 17 | 41275545 | 41275700 | ACACTGACGACATGGTTCTACATTAGTGGAGAGGGGGTTTCA | TACGGTAGCAGAGACTTGGTCTCCATCACTTGAAATGGCAAA | 156 | 53 | TTAGTGGAGAGGGGGTTTCACCATGTTGGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCTACCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATAAGCCACCGCCCTCGGCCTCATCCATGATTTTATTTTGCCATTTCAAGTGATGG |
| BRCA2 | BRCA2_Promoter_1 | 13 | 32888507 | 32888705 | ACACTGACGACATGGTTCTACACACCTTCTGGAAGCAGCAA | TACGGTAGCAGAGACTTGGTCTCATCTTTTGCATTCTTAGGATTCGG | 199 | 47 | CACCTTCTGGAAGCAGCAAGGCCCCCATGGGAGCAACTCTCACTGAATCCATTTGAAGGTTTTGTAGGTCTTACAACAAACCCTATTCAGCCTTGTATTAGGCATGTTACAGAACCAACGAATTCGGAGATGAAGTCAGGTCTTCCAGTTCAGCCTGCGAGGAAGACAGGTGATCCGAATCCTAAGAATGCAAAAGATG |
| BRCA2 | BRCA2_Promoter_3 | 13 | 32888996 | 32889147 | ACACTGACGACATGGTTCTACAaaaagcaaaaGATACTACCAAGCC | TACGGTAGCAGAGACTTGGTCTTTTAGTTCCAGTAGCTGTTCTGC | 152 | 46 | aaaagcaaaaGATACTACCAAGCCCTGCGGAGCAAGGTACCTCACACTTCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGGGCTCGGAGGTCTTGAACACCTGCTACCCAATAGCAGAACAGCTACTGGAACTAAA | One primer sits in the repeat region |
| BRCA2 | BRCA2_Promoter_6 | 13 | 32889044 | 32889230 | ACACTGACGACATGGTTCTACATCATGAGCGAGTTAAGATGGGTT | TACGGTAGCAGAGACTTGGTCTAAAAGCTTAGAGTGGTCGGTGTG | 187 | 46 | TCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGGGCTCGGAGGTCTTGAACACCTGCTACCCAATAGCAGAACAGCTACTGGAACTAAAATCCTCTGATTTCAAATAACAGCCCCGCCCACTACCACTAAGTGAAGTCATCCACAACCACACACCGACCACTCTAAGCTTTT |
| BRCA2 | BRCA2_prom_Stacey_1 | 13 | 32889175 | 32889357 | ACACTGACGACATGGTTCTACACCCACTACCACTAAGTGAAGTCAT | TACGGTAGCAGAGACTTGGTCTTTTTGCTCCAGCTCATGTTTGG | 183 | 50 | CCCACTACCACTAAGTGAAGTCATCCACAACCACACACCGACCACTCTAAGCTTTTGTAAGATCGGCTCGCTTTGGGGAACAGGTCTTGAGAGAACATCCCTTTTAAGGTCAGAACAAAGGTATTTCATAGGTCCCAGGTCGTGTCCCGAGGGCGCCCACCCAAACATGAGCTGGAGCAAAAA |
| BRCA2 | BRCA2_prom_Stacey_2 | 13 | 32889210 | 32889390 | ACACTGACGACATGGTTCTACACCGACCACTCTAAGCTTTTGT | TACGGTAGCAGAGACTTGGTCTCCCTATGCCTACTCCAAGTCCC | 181 | 52 | CACCGACCACTCTAAGCTTTTGTAAGATCGGCTCGCTTTGGGGAACAGGTCTTGAGAGAACATCCCTTTTAAGGTCAGAACAAAGGTATTTCATAGGTCCCAGGTCGTGTCCCGAGGGCGCCCACCCAAACATGAGCTGGAGCAAAAAGAGGGATGGGGGACTTGGAGTAGGCATAGGG |
| BRCA2 | BRCA2_Promoter_Combined_7 | 13 | 32889335 | 32889530 | ACACTGACGACATGGTTCTACACCAAACATGAGCTGGAGCAAAAA | TACGGTAGCAGAGACTTGGTCTATTTCTCAGTGTGGCGAAAGGAA | 196 | 54 | CCAAACATGAGCTGGAGCAAAAAGAAAGGGATGGGGGACTTGGAGTAGGCATAGGGGCGGCCCCTCCAAGCAGGGTGGCCTGGGACTCTTAAGGGTCAGCGAGAAGAGAACACACACTCCAGCTCCCGCTTTATTCGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCCTTTCGCCACACTGAGAAAT |
| BRCA2 | BRCA2_Promoter_10 | 13 | 32889458 | 32889650 | ACACTGACGACATGGTTCTACATCCCGCTTTATTCGGTCAGATAC | TACGGTAGCAGAGACTTGGTCTGCCTCTGCCGCCTAGTT | 193 | 62 | TCCCGCTTTATTCGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCCTTTCGCCACACTGAGAAATACCCGCAGCGGCCCACCCAGGCCTGACTTCCGGGTGGTGCGTGTGCTGCGTGTCGCGTCACGGCGTCACGTGGCCAGCGCGGGCTTGTGGCGCGAGCTTCTGAAACTAGGCGGCAGAGGC |
| BRCA2 | BRCA2_Promoter_Combined_10 | 13 | 32889508 | 32889703 | ACACTGACGACATGGTTCTACATTCCTTTCGCCACACTGAGAAAT | TACGGTAGCAGAGACTTGGTCTCCGCAAAAGACACCCGAGG | 196 | 67 | TTCCTTTCGCCACACTGAGAAATACCCGCAGCGGCCCACCCAGGCCTGACTTCCGGGTGGTGCGTGTGCTGCGTGTCGCGTCACGGCGTCACGTGGCCAGCGCGGGCTTGTGGCGCGAGCTTCTGAAACTAGGCGGCAGAGGCGGAGCCGCTGTGGCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGCGG |
| BRCA2 | BRCA2_5_UTR__exon_1__2 | 13 | 32889663 | 32889835 | ACACTGACGACATGGTTCTACAGCACTGCTGCGCCTCT | TACGGTAGCAGAGACTTGGTCTCTCGTCCCAACCCACTACCA | 173 | 62 | GCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGCGGCGGTGGGTCGCCGCCGGGAGAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTCAGCTTACTCCGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTAGTGGGTTGGGACGAG |
| BRCA2 | BRCA2_prom_Stacey_7 | 13 | 32889723 | 32889921 | ACACTGACGACATGGTTCTACAGAAGCGTGAGGGGACAGATTT | TACGGTAGCAGAGACTTGGTCTAGAGACAAAAGGGCAAGAAGCC | 199 | 63 | GAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTCAGCTTACTCCGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTAGTGGGTTGGGACGAGCGGCGTCTTCCGCAGTCCCAGTCCAGCGTGGCGGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTTGTCTCT |
| BRCA2 | BRCA2_prom_Stacey_8 | 13 | 32889839 | 32890018 | ACACTGACGACATGGTTCTACAGTCTTCCGCAGTCCCAGTC | TACGGTAGCAGAGACTTGGTCTGAAATGGAGACCCAGGGAAGG | 180 | 64 | GTCTTCCGCAGTCCCAGTCCAGCGTGGCGGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTTGTCTCTGCCAACCCCCACCCATGCCTGAGAGAAAGGTCCTTGCCCGAAGGCAGATTTTCGCCAAGCAAATTCGAGCCCCGCCCCTTCCCTGGGTCTCCATTTC |
| BRCA2 | BRCA2_1 | 13 | 32890522 | 32890720 | ACACTGACGACATGGTTCTACATCCCTGTGTAAGTGCATTTTGGT | TACGGTAGCAGAGACTTGGTCTTTTAGAAAACACTTTCTCGGTGTAAT | 199 | 34 | TCCCTGTGTAAGTGCATTTTGGTCTTCTGTTTTGCAGACTTATTTACCAAGCATTGGAGGAATATCGTAGGTAAAAATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGGTATTGACAAATTTTATATAACTTTATAAATTACACCGAGAAAGTGTTTTCTAAAA |
| BRCA2 | BRCA2_2 | 13 | 32893174 | 32893358 | ACACTGACGACATGGTTCTACATCACTGGTTAAAACTAAGGTGGGA | TACGGTAGCAGAGACTTGGTCTTAAGATGGTTTCCTTTGTGGAGT | 185 | 32 | TCACTGGTTAAAACTAAGGTGGGATTTTTTTTTTAAATAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAAT |

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| | | | | | | | | TCTGAACCTGCAGAAGAATCTGAACATAAAAACAACAATTACGAACCAAA CCTATTTAAAACTCCACAAAGGAAACCATCTTA | |
| BRCA2 | BRCA2_3 | 13 | 32893249 | 32893426 | ACACTGACGACATGGTTCTA CACTTTCTTCAGAAGCTCCA CCCTA | TACGGTAGCAGAGACTTGGTCTG AGATTGGTACAGCGGCAGAG | 178 | 39 | CTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATCTGA ACATAAAAACAACAATTACGAACCAAACCTATTTAAAACTCCACAAAGGA AACCATCTTATAATCAGCTGGCTTCAACTCCAATAATATTCAAAGAGCAA GGGCTGACTCTGCCGCTGTACCAATCTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_4 | 13 | 32893336 | 32893492 | ACACTGACGACATGGTTCTA CAACTCCACAAAGGAAACCA TCTTA | TACGGTAGCAGAGACTTGGTCTC TCCCCAGTCTACCATATTGCAT | 157 | 39 | ACTCCACAAAGGAAACCATCTTATAATCAGCTGGCTTCAACTCCAATAAT ATTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTCCTGTAAAA GAATTAGATAAATTCAAATTAGACTTAGGTAAGTAATgcaatatggtagactgggg ag | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_1 | 13 | 32897972 | 32898163 | ACACTGACGACATGGTTCTA CAACTTAATGCCCTGGAGAG TCAAA | TACGGTAGCAGAGACTTGGTCTA GACAAAGTGAGTTGCAGACAGTA | 192 | 29 | ACTTAATGCCCTGGAGAGTCAAATATAATCTACTCTAATACAGAAAATAG AAATATTGAAAAACTGTAAATTGGATTTCATATTGTTAAAGCCACCTATAG CTTTAGAAACTCTGAACATTATTTTCTTAGAAAATGGATGTGTTCAATAAG AATAGAAATTATGTATTACTGTCTGCAACTCACTTTGTCT | |
| BRCA2 | BRCA2_Intron_3_2 | 13 | 32898044 | 32898221 | ACACTGACGACATGGTTCTA CAGGATTTCATATTGTTAAAG CCACCTAT | TACGGTAGCAGAGACTTGGTCTT GTCTGGTATATTAGTCACTCCTG AA | 178 | 30 | GGATTTCATATTGTTAAAGCCACCTATAGCTTTAGAAACTCTGAACATTAT TTTCTTAGAAAATGGATGTGTTCAATAAGAATAGAAATTATGTATTACTGT CTGCAACTCACTTTGTCTAATTATATCCAatttattcatccagtcaatatttcaggagtgact aatataccagaca | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_3 | 13 | 32898141 | 32898311 | ACACTGACGACATGGTTCTA CAACTGTCTGCAACTCACTT TGTCT | TACGGTAGCAGAGACTTGGTCTA CACTGTTCTTTTTCCCCCTACT | 171 | 37 | ACTGTCTGCAACTCACTTTGTCTAATTATATCCAatttattcatccagtcaatatttcag gagtgactaatataccagacatttttgtagttgctagggatacagtgacaaataagacaaaatctctacctca gattgctcacagcctagtaggggaaaaagaacagtgt | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_4 | 13 | 32898184 | 32898355 | ACACTGACGACATGGTTCTA CATCCAGTCAATATTTCAGG AGTGACTAA | TACGGTAGCAGAGACTTGGTCTT TAAGTGTTTGCCCCCCTATGTG | 172 | 40 | tccagtcaatatttcaggagtgactaatataccagacatttttgtagttgctagggatacagtgacaaataag acaaaatctctacctcagattgctcacagcctagtaggggaaaaagaacagtgtatgatcaaactcttca gggaacacataggggggcaaacacttaa | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_5 | 13 | 32898267 | 32898457 | ACACTGACGACATGGTTCTA CATACCTCAGATTGCTCACA GCCTA | TACGGTAGCAGAGACTTGGTCTG CTGTTTCCCCTTCTTTGCTTTT | 191 | 44 | tacctcagattgctcacagcctagtaggggaaaaagaacagtgtatgatcaaactcttcagggaacaca taggggggcaaacacttaatcttaccttagggatcactacagttttctggaggaggtagtttctaaatggaag cctgaaagagttgttccaggtcaagaaaagcaaagaaggggaaacagc | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_6 | 13 | 32898366 | 32898559 | ACACTGACGACATGGTTCTA CAGGGATCACTACAGTTTTC TGGAGG | TACGGTAGCAGAGACTTGGTCTA ATTTTTATGATGCCATTCTTTTAC AGTC | 194 | 38 | gggatcactacagttttctggaggaggtagtttctaaatggaagcctgaaagagttgttccaggtcaagaaa agcaaagaaggggaaacagcttgtacaaagtcctagaggttaaagaaaacattctttcaggatatgcaa atggttgggtatgggtaaaaagtagactgtaaaagaatggCATCATAAAAATT | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_7 | 13 | 32898426 | 32898622 | ACACTGACGACATGGTTCTA CACAGGTCAAGAAAAGCAAA GAAGGG | TACGGTAGCAGAGACTTGGTCTT TTCTTCATTTTTAATTTTTGTGGG TACAT | 197 | 30 | caggtcaagaaaagcaaagaaggggaaacagcttgtacaaagtcctagaggttaaagaaaacattctttt caggatatgcaaatggttgggtatgggtaaaaagtagactgtaaaagaatggCATCATAAAAATT AAGTAAATTGTCAcataaatatatatattttcttatgtacccacaaaaattaaaaaTGAAGAAA | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_3_8 | 13 | 32898527 | 32898716 | ACACTGACGACATGGTTCTA CAAGTAGACTGTAAAAGAAT GGCATCA | TACGGTAGCAGAGACTTGGTCTT GACAATATCACTTGTGCTAAAAAC CT | 190 | 27 | agtagactgtaaaagaatggCATCATAAAAATTAAGTAAATTGTCAcataaatatatatattttcttatgtacccacaaaaattaaaaaTGAAGAAATTAAGTAAATTGTCACATCATAAAAATT TACTATGGAGTTTGACTTGATCTTGAAAAGTAAGATCTTGAAAGGTTTTTA GCACAAGTGATATTGTCA | One primer sits in the repeat region |
| BRCA2 | BRCA2_5 | 13 | 32899149 | 32899334 | ACACTGACGACATGGTTCTA CACCAAAGAATGCAAATTTAT AATCCAGAGT | TACGGTAGCAGAGACTTGGTCTA GCTTCATCATACCTTTCACTAAGA C | 186 | 34 | ccaaagaatgcaaatttataatcCAGAGTATATACATTCTCACTGAATTATTGTACTG TTTCAGGAAGGAATGTTCCCAATAGTAGACATAAAAGTCTTCGCACAGTG AAAACTAAAATGGATCAAGCAGATGATGTTTCCTGTCCACTTCTAAATTC TTGTCTTAGTGAAAGGTATGATGAAGCt | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_6 | 13 | 32899280 | 32899435 | ACACTGACGACATGGTTCTA CATGATGTTTCCTGTCCACTT CTAAA | TACGGTAGCAGAGACTTGGTCTT CTACCAGGCTCTTAGCCAAAAT | 156 | 28 | TGATGTTTCCTGTCCACTTCTAAATTCTTGTCTTAGTGAAAGGTATGATGA AGCtattatattaaaatatttaaatGAAACATTTTCCTACATATATTTGTTCTATAAAG ATGAATCTGATTTTTATGCTAATATTTTGGCTAAGAGCCTGGTAGA | |
| BRCA2 | BRCA2_7 | 13 | 32900202 | 32900400 | ACACTGACGACATGGTTCTA CAAAAATAACCTAAGGGATT TGCTTTGT | TACGGTAGCAGAGACTTGGTCTT GAAACAAACTCCCACATACCACT | 199 | 30 | AAAATAACCTAAGGGATTTGCTTTGTTTTATTTTAGTCCTGTTGTTCTACA ATGTACACATGTAACACCACAAAGAGATAAGTCAGGTATGATTAAAAACA ATGCTTTTTATTCTTAGAATACTAGAAATGTTAATAAAAATAAAACTTAACA ATTTTCCCCTTTTTTTACCCCCAGTGGTATGTGGGAGTTTGTTTCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_8 | 13 | 32900331 | 32900527 | ACACTGACGACATGGTTCTA CATGTTAATAAAAATAAAACT TAACAATTTTCCCCTT | TACGGTAGCAGAGACTTGGTCTT GAGGCAGAATGCTAGGTACAGA | 197 | 33 | TGTTAATAAAAATAAAACTTAACAATTTTCCCCTTTTTTTACCCCCAGTGG TATGTGGGAGTTTGTTTCATACACCAAAGTTTGTGAAGGTAAATATTCTA CCTGGTTTATTTTTATGACTTAGTAATTGAGAATTTGACAATAGCGTTATA CCTTTGCCCTGAGATTTACAAATCTGTACCTAGCATTCTGCCTCA | |
| BRCA2 | BRCA2_9 | 13 | 32900545 | 32900728 | ACACTGACGACATGGTTCTA CAACGTTAAGTGAAATAAAG AGTGAATGAA | TACGGTAGCAGAGACTTGGTCTG GTGGGTGGTGTAGCTAAAGA | 184 | 37 | ACGTTAAGTGAAATAAAGAGTGAATGAAAAAATAATATCCTTAATGATCA GGGCATTTCTATAAAAAATAAACTATTTTCTTTCCTCCCAGGGTCGTCAG ACACCAAAACATATTTCTGAAAGTCTAGGAGCTGAGGTGGATCCTGATAT GTCTTGGTCAAGTTCTTTAGCTACACCACCCACC | |
| BRCA2 | BRCA2_10 | 13 | 32900618 | 32900797 | ACACTGACGACATGGTTCTA CATATTTTCTTTCCTCCCAGG GTCGT | TACGGTAGCAGAGACTTGGTCTT CAACCTCATCTGCTCTTTCTTG | 180 | 41 | TATTTTCTTTCCTCCCAGGGTCGTCAGACACCAAAACATATTTCTGAAAG TCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTA CACCACCCACCCTTAGTTCTACTGTGCTCATAGGTAATAATAGCAAATGT GTATTTACAAGAAAGAGCAGATGAGGTTGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_11 | 13 | 32903475 | 32903668 | ACACTGACGACATGGTTCTA CATGTGTCATGTAATCAAATA GTAGATGTG | TACGGTAGCAGAGACTTGGTCTA GCAATTTCAACAGTCTAATCAATG TC | 194 | 29 | TGTGTCATGTAATCAAATAGTAGATGTGCTTTTTGATGTCTGACAAAAAAT AAGTTTTTGCATTCTAGTGATAATATACAATACACATAAATTTTTATCTTAC AGTCAGAAATGAAGAAGCATCTGAAACTGTATTTCCTCATGATACTACTG CTGTAAGTAAATATGACATTGATTAGACTGTTGAAATTGCT | |
| BRCA2 | BRCA2_Intron_8_1 | 13 | 32904422 | 32904620 | ACACTGACGACATGGTTCTA CATGTGACAGCAAAACCAGC TCATA | TACGGTAGCAGAGACTTGGTCTG GCCCCAAAGCACAAGTATAATG | 199 | 38 | tgtgacagcaaaaccagctcatatgtctttctccttcacaatctcacagatagatttgttcttaccatagatgtcg cagtacaatttttttccttttcctttaagtcgagaactttcactgtttcaattaaaggaagcactttatggcttcttttttgg catatttgaattgccagcatcattatactttgtgctttggggcc | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_8_2 | 13 | 32904478 | 32904657 | ACACTGACGACATGGTTCTA CATGTTCTTACCATAGATGTC GCAGT | TACGGTAGCAGAGACTTGGTCTT GCTTGTGTTCAAGTCACCCTTA | 180 | 36 | tgttcttaccatagatgtcgcagtacaatttttttccttttcctttaagtcgagaactttcactgtttcaattaaaggaa gcactttatggcttcttttttggcatatttgaattgccagcatcattatactttgtgctttggggccattgttaagtaaaa taagggtgacttgaacacaagca | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_8_3 | 13 | 32904600 | 32904770 | ACACTGACGACATGGTTCTA CATTATACTTGTGCTTTGGG GCCAT | TACGGTAGCAGAGACTTGGTCTA CTTGGGACATGAATCATCCCTT | 171 | 43 | ttatacttgtgctttggggccattgttaagtaaaataagggtgacttgaacacaagcactgtggtaccacaata gccgatctgataaccaagacaactactaagtgactaataggtgggtaccatatacagcctggatacgctg gacaaagggatgattcatgtcccaagt | Two primers sits in the repeat region |

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| BRCA2 | BRCA2_Intron_8_4 | 13 | 32904673 | 32904852 | ACACTGACGACATGGTTCTACAAGCCGATCTGATAACCAAGACAA | TACGGTAGCAGAGACTTGGTCTCTTGCACCACTAGGATGTGGAAA | 180 | 43 | agccgatctgataaccaagacaactactaagtgactaataggtgggtaccatatacagcctggatacgctggacaaagggatgattcatgtcccaagtgggatggagcaagatggtgcaagttttttttctccatttccattttccttctaagatttccacatcctagtggtgcaag | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_8_5 | 13 | 32904749 | 32904920 | ACACTGACGACATGGTTCTACAAGGGATGATTCATGTCCCAAGTG | TACGGTAGCAGAGACTTGGTCTGGAAAATTCCAGAAGTAAGCAATTAGT | 172 | 38 | agggatgattcatgtcccaagtgggatggagcaagatggtgcaagttttttttctccatttccattttcctttcctaagatttccacatcctagtggtgcaagatttcatcacactactcaggatgacacacaatttaaaacttactaattgcttacttctggaattttcc | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_8_6 | 13 | 32904844 | 32905015 | ACACTGACGACATGGTTCTACATGGTGCAAGATTTCATCACACTA | TACGGTAGCAGAGACTTGGTCTTCAATGCACATATAGTAGTAGTCCC | 172 | 35 | tggtgcaagatttcatcacactactcaggatgacacacaatttaaaacttactaattgcttacttctggaattttccattaaaaattttggacctaggttgattgcagataactgaaatcaccaaaagtgaaaccatggataaggggactactACTATATGTGCATTGA | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_8_7 | 13 | 32904887 | 32905077 | ACACTGACGACATGGTTCTACAAAAACTTACTAATTGCTTACTTCTGGAAT | TACGGTAGCAGAGACTTGGTCTTGGAAAAATAGCTTTTCACATTCTGC | 191 | 31 | aaaacttactaattgcttacttctggaattttccattaaaaattttggacctaggttgattgcagataactgaaatcaccaaaagtgaaaccatggataaggggggactactACTATATGTGCATTGAGAGTTTTTATACTAGTGATTTTAAACTATACTAGTGATTTTAAACTATAATTTTTGCAGAATGTGAAAAGCTATTTTTCCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_12 | 13 | 32904990 | 32905188 | ACACTGACGACATGGTTCTACAGGGGACTACTACTATATGTGCATTGA | TACGGTAGCAGAGACTTGGTCTTCAACTAAACAGAGGACTTACCATGA | 199 | 33 | ggggactactACTATATGTGCATTGAGAGTTTTTATACTAGTGATTTTAAACTATAATTTTTGCAGAATGTGAAAAGCTATTTTTCCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGCTTCTGTGACAGACAGTGAAAACACAAATCAAAGAAGCTGCAAGTCATGGTAAGTCCTCTGTTTAGTTGAACTACAGGTTTTTTTGTTGTTGTTGTTTTGACTGTGACAGACAGTGAAAACACAAATCAAAGAGAAGCTGCAAGTCATGGTTTTTTTTTTTTGAGGTGGAGTCTTGCTCTGTCACCCGTGATCTCGGTTTACCGCAACCT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_126 | 13 | 32905120 | 32905279 | ACACTGACGACATGGTTCTACACTGTGACAGACAGTGAAAACACA | TACGGTAGCAGAGACTTGGTCTAGGTTGCGGTAAACCGAGAT | 160 | 40 | | |
| BRCA2 | BRCA2_13 | 13 | 32906365 | 32906537 | ACACTGACGACATGGTTCTACATGGCTTATAAAATATTAATGTGCTTCTGT | TACGGTAGCAGAGACTTGGTCTAACTATCTTCTTCAGAGGTATCTACAAC | 173 | 32 | TGGCTTATAAAATATTAATGTGCTTCTGTTTTATACTTTAACAGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAAGACCACATTGGAAAGTCAATGCCAAATGTCCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_14 | 13 | 32906405 | 32906593 | ACACTGACGACATGGTTCTACAACAGGATTTGGAAAAACATCAGGG | TACGGTAGCAGAGACTTGGTCTGCTAGTTCTTACTTTTTGTAGATTTTTGTTCT | 189 | 31 | ACAGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAAGACCACATTGGAAAGTCAATGCCAAATGTCCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAAATCTACAAAAAGTAAGAACTAGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_15 | 13 | 32906502 | 32906695 | ACACTGACGACATGGTTCTACAATGAAACAGTTGTAGATACCTCTGAA | TACGGTAGCAGAGACTTGGTCTTGGTTCCACTTCAGATACAAATGAGT | 194 | 29 | ATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAAATCTACAAAAAGTAAGAACTAGCAAGACTAGGAAAAAAATTTTCCATGAAGCAAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_16 | 13 | 32906614 | 32906786 | ACACTGACGACATGGTTCTACACCATGAAGCAAACGCTGATGAAT | TACGGTAGCAGAGACTTGGTCTAAGACGGTACAACTTCCTTGGAG | 173 | 36 | CCATGAAGCAAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAAAAATACTCATTTGTATCTGAAGTGGAAGTGACAAAAGATTCAAATGTAGCAAATCAGAAGCCCTTTGAGAGTGGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_17 | 13 | 32906677 | 32906859 | ACACTGACGACATGGTTCTACATGTATCTGAAGTGGAACCAAATGA | TACGGTAGCAGAGACTTGGTCTTGCAATAGGGGTATTTTCTCCAT | 183 | 42 | TGTATCTGAAGTGGAACCAAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGAAGCCCTTTGAGAGTGGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGATGGAGAAAATACCCCTATTGCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_18 | 13 | 32906777 | 32906973 | ACACTGACGACATGGTTCTACAGTACCGTCTTTGGCCTGTGAATG | TACGGTAGCAGAGACTTGGTCTGGTAGGCTAGAAATACGTGGCAAA | 197 | 39 | GTACCGTCTTTGGCCTGTGAATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGATGGAGAAAATACCCCTATTGCATAATTTCTTCATGTGACCAAAATATTTCAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGAATTCTTTGCCACGTATTTCTAGCCTACC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_19 | 13 | 32906851 | 32907049 | ACACTGACGACATGGTTCTACACCTATTGCATATTTCTTCATGTGACC | TACGGTAGCAGAGACTTGGTCTTGTATGAGATTCAAGATGCTGCT | 199 | 34 | CCTATTGCATATTTCTTCATGTGACCAAAATATTTCAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGAATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATAAGAGAGATGAAGAGCAGCATCTTGAATCTCATACAGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGAACTTCTCCAGTGGCTTCTTCATTTCAGGGTA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_20 | 13 | 32906946 | 32907116 | ACACTGACGACATGGTTCTACAATTCTTTGCCACGTATTTCTAGCC | TACGGTAGCAGAGACTTGGTCTTACCCTGAAATGAAGAAGCCACT | 171 | 40 | TTCTTGCAGTAAAGCAGGCAATATCTGGAACTTCTCCAGTGGCTTCTTCATTTTCAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAGAGACTTTCAATGCAAGTTTTTCAGGTCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_21 | 13 | 32907057 | 32907233 | ACACTGACGACATGGTTCTACATTCTTGCAGTAAAGCAGGCAATA | TACGGTAGCAGAGACTTGGTCTGTCCACTTTCAGAGGCTTCAGTT | 177 | 37 | TCCAGTGGCTTCTTCATTTCAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAGAGACTTTCAATGCAAGTTTTTCAGGTCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACAGAAGGAGGACTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_22 | 13 | 32907091 | 32907270 | ACACTGACGACATGGTTCTACATCCAGTGGCTTCTTCATTTCAGG | TACGGTAGCAGAGACTTGGTCTGAGTCCTCCTTCTGTGAGCAAAC | 180 | 37 | TGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_23 | 13 | 32907186 | 32907361 | ACACTGACGACATGGTTCTACATGACTGATCCAAACTTTAAAAAGAAACT | TACGGTAGCAGAGACTTGGTCTAGTGGATATTAAACCTGCATTCTTCA | 176 | 40 | GAAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_24 | 13 | 32907264 | 32907455 | ACACTGACGACATGGTTCTACAAGGACTCCTTATGTCCAAATTTAATTGAT | TACGGTAGCAGAGACTTGGTCTTTAGTTCTGATTTTTGGTCTTTCGG | 192 | 32 | AGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACTTTGAAAAAGAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAAAATAAAGGAAAAAAATACCGAAAGACCAAAAATCAGAACTAATTAACTGTTCAGCCCAGTTTGAAGCAAATGCTTTTGAAGCACCACTTACATTTGCAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_25 | 13 | 32907328 | 32907512 | ACACTGACGACATGGTTCTACATGTAGCTTTGAAGAATGCAGGTTT | TACGGTAGCAGAGACTTGGTCTTTGCAAATGTAAGTGGTGCTTCA | 185 | 30 | | |

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| BRCA2 | BRCA2_26 | 13 | 32907463 | 32907643 | ACACTGACGACATGGTTCTACATTCAGCCCAGTTTGAAGCA | TACGGTAGCAGAGACTTGGTCTGATGATGCCTAAGATTAAATATAAGATATGAAGA | 181 | 31 | TTCAGCCCAGTTTGAAGCAAATGCTTTTGAAGCACCACTTACATTTGCAAATGCTGATTCAGGTACCTCTGTCTTTTTTTTTTTGTAAATAGTACATATAGTTTTATAGATGACGATTCCTTCTGTGTTTTTTTCTGCTTTTTAAAATCTTCATATCTTATATTTAATCTTAGGCATCATC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_27 | 13 | 32910305 | 32910494 | ACACTGACGACATGGTTCTACAactgtgcccAAACACTACCTT | TACGGTAGCAGAGACTTGGTCTTCAGAATTGTCCCAAAAGAGCTA | 190 | 33 | actgtgcccAAACACTACCTTTTTAACTTAGTGAAAAATATTTAGTGAATGTGATTGATGGTACTTTAATTTTGTCACTTTGTGTTTTTATGTTTAGGTTTATTGCATTCTTCTGTGAAAAGAAGCTGTTCACAGAATGATTCTGAAGAACCAACTTTGTCCTTAACTAGCTCTTTTGGGACAATTCTGA | One primer sits in the repeat region |
| BRCA2 | BRCA2_28 | 13 | 32910395 | 32910590 | ACACTGACGACATGGTTCTACATGTTTAGGTTTATTGCATTCTTCTGTGA | TACGGTAGCAGAGACTTGGTCTACTGTAGTTTTTCCTTATTACATTTTGCT | 196 | 32 | TGTTTAGGTTTATTGCATTCTTCTGTGAAAAGAAGCTGTTCACAGAATGATTCTGAAGAACCAACTTTGTCCTTAACTAGCTCTTTTGGGACAATTCTGAGGAAATGTTCTAGAAATGAAACATGTTCTAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAATAAGGAAAAACTACAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_29 | 13 | 32910464 | 32910654 | ACACTGACGACATGGTTCTACATCCTTAACTAGCTCTTTTGGGACA | TACGGTAGCAGAGACTTGGTCTGGATCATTTTCACACTGTCCTTCC | 191 | 35 | TCCTTAACTAGCTCTTTTGGGACAATTCTGAGGAAATGTTCTAGAAATGAAACATGTTCTAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAATAAGGAAAAACTACAGTTATTTATTACCCCAGAAGCTGATTCTCTGTCATGCCTGCAGGAAGGACAGTGTGAAAATGATCC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_30 | 13 | 32910603 | 32910766 | ACACTGACGACATGGTTCTACACAGAAGCTGATTCTCTGTCATGC | TACGGTAGCAGAGACTTGGTCTACTTTTCTGGGATTGAAAGTCAGTAT | 164 | 40 | CAGAAGCTGATTCTCTGTCATGCCTGCAGGAAGGACAGTGTGAAAATGATCCAAAAAGCAAAAAAGTTTCAGATATAAAAGAAGAGGTCTTGGCTGCAGCATGTCACCCAGTACAACAATCCCAGAAAAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_31 | 13 | 32910671 | 32910842 | ACACTGACGACATGGTTCTACATCAGATATAAAAGAAGAGGTCTTGGC | TACGGTAGCAGAGACTTGGTCTTGACTAGGTTTGACAGAACATCC | 172 | 38 | TCAGATATAAAAGAAGAGGTCTTGGCTGCAGCATGTCACCCAGTACAACATTCAAAAGTGGAATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAATGCCAGCACTCTTATTTTAACTCCTACTTCCAAGGATGTTCTGTCAAACC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_32 | 13 | 32910787 | 32910961 | ACACTGACGACATGGTTCTACATGCCAGCACTCTTATTTTAACTCCT | TACGGTAGCAGAGACTTGGTCTAGCACATACATCTTGATTCTTTTCCA | 175 | 35 | TAGTCATGATTTCTAGAGGCAAAGAATCATACAAAATGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAATATTCCCATGGAAAAGAATCAAGATGTATGTGCT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_33 | 13 | 32910870 | 32911041 | ACACTGACGACATGGTTCTACAAAATGTCAGACAAGCTCAAAGGT | TACGGTAGCAGAGACTTGGTCTTGTACCTTTCTTGAAGGTGATGCT | 172 | 33 | AAATGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAATATTCCCATGGAAAAGAATCAAGATGTATGTGCTTTAAATGAAAATTATAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATGAGAGTAGCATCACCTTCAAGAATGGTACAATTCAACCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_34 | 13 | 32910936 | 32911134 | ACACTGACGACATGGTTCTACATGGAAAAGAATCAAGATGTATGTGCT | TACGGTAGCAGAGACTTGGTCTTCTTCAGAGTCTGGATTGACAGTTAT | 199 | 32 | TGGAAAAGAATCAAGATGTATGTGCTTTAAATGAAAATTATAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATGAGAGTAGCATCACCTTCAAGAAAGGTACAATTCAACCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGACAATGAGAATAATTTTG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_35 | 13 | 32911048 | 32911246 | ACACTGACGACATGGTTCTACACCAAAACACAAATCTAAGAGTAATCCA | TACGGTAGCAGAGACTTGGTCTGTTTACACAAGTCAAGTCTGTTTCA | 199 | 31 | CCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGACAATGAGAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGCTTTAGGAAATACTAAGGAACTTCATGAAACAGACTTGACTTGTGTAAACGAACCCATTTTCAAGAACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAAGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_36 | 13 | 32911114 | 32911305 | ACACTGACGACATGGTTCTACATGTCAATCCAGACTCTGAAGAACT | TACGGTAGCAGAGACTTGGTCTGCTTGTTTATCACCTGTGTCTCC | 192 | 35 | CAGACTTGACTTGTGTAAACGAACCCATTTTCAAGAACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAAGCAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAAATAGTGTAAAGCAGCATATAAAAATGATGTTCTTGCAGAGGAGAACAAAAATAGTGTAAAGCAGCATATAAAAATGACTCTAGGTCAAGATTTAAAATCGGACATCTCCTTGAATATAGATAAAATACCAGAAAAAAATAATGATTACATGAACAAATTCAAATCACAGTTTTGGAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_37 | 13 | 32911227 | 32911397 | ACACTGACGACATGGTTCTACACAGACTTGACTTGTGTAAACGAACC | TACGGTAGCAGAGACTTGGTCTGACCTAGAGTCATTTTTATATGCTGCTTT | 171 | 36 | TTATATGGAGACACAGGTGATAAACAAGCAACCCAAGTGTCAATTAAAAAATATAAAAATGACTCTAGGTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_38 | 13 | 32911338 | 32911529 | ACACTGACGACATGGTTCTACAATGTTCTTGCAGAGGAGAACAAA | TACGGTAGCAGAGACTTGGTCTAAGCTGTTCTGAAGCTACCTC | 192 | 34 | GAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAAGCAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_39 | 13 | 32911416 | 32911569 | ACACTGACGACATGGTTCTACATCTCCTTGAATATAGATAAAATACCAGAAAAAA | TACGGTAGCAGAGACTTGGTCTTTCTTAATGTTATGTTCAGAGAGCTTG | 154 | 33 | TCTCCTTGAATATAGATAAAATACCAGAAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACAGTTTTGGAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAGAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_40 | 13 | 32911509 | 32911679 | ACACTGACGACATGGTTCTACAGAGGTAGCTTCAGAACAGCTTCA | TACGGTAGCAGAGACTTGGTCTGAGGCTTGCTCAGTTTCTTTTGATT | 171 | 34 | GAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAGCAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTCAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAGCAAAATGTTCTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_41 | 13 | 32911535 | 32911731 | ACACTGACGACATGGTTCTACAAAGGAAATCAAGCTCTCTGAACA | TACGGTAGCAGAGACTTGGTCTTCAGAAACAACTACACTACTCTGTAAA | 197 | 32 | CAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGAGTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_42 | 13 | 32911651 | 32911821 | ACACTGACGACATGGTTCTACAAGATAATCAAAAGAAACTGAGCAAGC | TACGGTAGCAGAGACTTGGTCTTCTGCCTTTTGGCTAGGTG | 171 | 33 | AGATAATCAAAAGAAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGAGTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_43 | 13 | 32911752 | 32911942 | ACACTGACGACATGGTTCTACACCCCTCAGATGTTATTTTCCAAGC | TACGGTAGCAGAGACTTGGTCTAGTCATCTGGTTTTCAGGCACTT | 191 | 35 | CCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAATCAGGAAGTCAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAGTGCCTGAAAACCAGATGACT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_44 | 13 | 32911796 | 32911973 | ACACTGACGACATGGTTCTACAAATTTAACACCTAGCCAAAAGGC | TACGGTAGCAGAGACTTGGTCTCTCTGCATTCCTCAGAAGTGGTC | 178 | 35 | AATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAATCAGGAAGTCAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTA | Assays designed by relax mode and have no off-target hits |

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| | | | | | | | | | CATATTGCAGAAGAGTACATTTGAAGTGCCTGAAAACCAGATGACTATCT TAAAGACCACTTCTGAGGAATGCAGAG | |
| BRCA2 | BRCA2_45 | 13 | 32911913 | 32912084 | ACACTGACGACATGGTTCTA CAACATTTGAAGTGCCTGAA AACCA | TACGGTAGCAGAGACTTGGTCTT TTTCAACAGGCCAGCAAACTTC | 172 | 41 | ACATTTGAAGTGCCTGAAAACCAGATGACTATCTTAAAGACCACTTCTGA GGAATGCAGAGATGCTGATCTTCATGTCATAATGAATGCCCCATCGATT GGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAAAC GGAAGTTTGCTGGCCTGTTGAAAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_46 | 13 | 32912025 | 32912218 | ACACTGACGACATGGTTCTA CAGCAGCAAGCAATTTGAAG GTACA | TACGGTAGCAGAGACTTGGTCTA CTAAACAGTTTCACAGCTTTTTGC | 194 | 38 | GCAGCAAGCAATTTGAAGGTACAGTTGAAATTAAACGGAAGTTTGCTGG CCTGTTGAAAAATGACTGTAACAAAAGTGCTTCTGGTTATTTAACAGATG AAAATGAAGTGGGGTTTAGGGGCTTTTATTCTGCTCATGGCACAAAACT GAATGTTTCTACTGAAGCTCTGCAAAAAGCTGTGAAACTGTTTAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_47 | 13 | 32912129 | 32912305 | ACACTGACGACATGGTTCTA CAGAAGTGGGGTTTAGGGG CTTTTA | TACGGTAGCAGAGACTTGGTCTT GAAACAACAGAATCATGACATTTA CTT | 177 | 37 | GAAGTGGGGTTTAGGGGCTTTTATTCTGCTCATGGCACAAAACTGAATG TTTCTACTGAAGCTCTGCAAAAAGCTGTGAAACTGTTTAGTGATATTGAG AATATTAGTGAGGAAACTTCTGCAGAGGTACATCCAATAAGTTTATCTTC AAGTAAATGTCATGATTCTGTTGTTTCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_48 | 13 | 32912216 | 32912409 | ACACTGACGACATGGTTCTA CAAGTGATATTGAGAATATTA GTGAGGAAACT | TACGGTAGCAGAGACTTGGTCTA CAAAAGTGCCAGTAGTCATTTCA | 194 | 27 | AGTGATATTGAGAATATTAGTGAGGAAACTTCTGCAGAGGTACATCCAAT AAGTTTATCTTCAAGTAAATGTCATGATTCTGTTGTTTCAATGTTTAAGAT AGAAAATCATAATGATAAAACTGTAAGTGAAAAAAATAATAAATGCCAACT GATATTACAAAATAATATTGAAATGACTACTGGCACTTTTGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_49 | 13 | 32912285 | 32912479 | ACACTGACGACATGGTTCTA CATGTCATGATTCTGTTGTTT CAATGT | TACGGTAGCAGAGACTTGGTCTT CTACTGGCAGCAGTATATTTGTT | 195 | 26 | TGTCATGATTCTGTTGTTTCAATGTTTAAGATAGAAAATCATAATGATAAA ACTGTAAGTGAAAAAAATAATAAATGCCAACTGATATTACAAAATAATATT GAAATGACTACTGGCACTTTTGTTGAAGAAATTACTGAAAATTACAAGAG AAATACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_50 | 13 | 32912391 | 32912574 | ACACTGACGACATGGTTCTA CATGACTACTGGCACTTTTG TTGAAG | TACGGTAGCAGAGACTTGGTCTT GATCAGTAAATAGCAAGTCCGT | 184 | 30 | TGACTACTGGCACTTTTGTTGAAGAAATTACTGAAAATTACAAGAGAAAT ACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAATTCTCATAA CTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTCA TAAAGATGAAACGGACTTGCTATTTACTGATCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_51 | 13 | 32912431 | 32912629 | ACACTGACGACATGGTTCTA CACAAGAGAAATACTGAAAA TGAAGATAACAAAT | TACGGTAGCAGAGACTTGGTCTC TGAGTGTTTCCCTCCTTCATAA | 199 | 33 | CAAGAGAAATACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGAA ATTCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTG TTTGTATTCATAAAGATGAAACGGACTTGCTATTTACTGATCAGCACAAC ATATGTCTTAAATTATCTGGCCAGTTTATGAAGGAGGGAAACACTCAG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_52 | 13 | 32912534 | 32912717 | ACACTGACGACATGGTTCTA CATGTATTCATAAAGATGAAA CGGACTTG | TACGGTAGCAGAGACTTGGTCTA CTGTTCTTTATTTGAAGTATTACC ATGAC | 184 | 34 | TGTATTCATAAAGATGAAACGGACTTGCTATTTACTGATCAGCACAACAT ATGTCTTAAATTATCTGGCCAGTTTATGAAGGAGGGAAACACTCAGATTA AAGAAGATTTGTCAGATTTAACTTTTTTGGAAGTTGCGAAAGCTCAAGAA GCATGTCATGGTAATACTTCAAATAAAGAACAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_53 | 13 | 32912600 | 32912792 | ACACTGACGACATGGTTCTA CAGGCCAGTTTATGAAGGAG GGAAA | TACGGTAGCAGAGACTTGGTCTT CCCACTTGCAGTCTGAAAAAATG | 193 | 35 | GGCCAGTTTATGAAGGAGGGAAACACTCAGATTAAAGAAGATTTGTCAG ATTTAACTTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCATGGTAAT ACTTCAAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAA AGATTTTGAGACTTCTGATACATTTTTTCAGACTGCAAGTGGGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_54 | 13 | 32912680 | 32912872 | ACACTGACGACATGGTTCTA CAAGAAGCATGTCATGGTAA TACTTCAAA | TACGGTAGCAGAGACTTGGTCTA AAGTTATGCAATTCTTCTGGTTTC T | 193 | 30 | AGAAGCATGTCATGGTAATACTTCAAATAAAGAACAGTTAACTGCTACTA AAACGGAGCAAAATATAAAAGATTTTGAGACTTCTGATACATTTTTTCAGA CTGCAAGTGGGAAAAATATTAGTGTCGCCAAAGAGTCATTTAATAAAATT GTAAATTTCTTTGATCAGAAACCAGAAGAATTGCATAACTTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_55 | 13 | 32912788 | 32912986 | ACACTGACGACATGGTTCTA CATGGGAAAAATATTAGTGT CGCCAAAG | TACGGTAGCAGAGACTTGGTCTA CCAACTGGGACACTTTCTTTCA | 199 | 30 | TGGGAAAAATATTAGTGTCGCCAAAGAGTCATTTAATAAAATTGTAAATTT CTTTGATCAGAAACCAGAAGAATTGCATAACTTTTCCTTAAATTCTGAATT ACATTCTGACATAAGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAA CAGACATAGTTAAACACAAAATACTGAAAGAAAGTGTCCCAGTTGGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_56 | 13 | 32912851 | 32913037 | ACACTGACGACATGGTTCTA CAACCAGAAGAATTGCATAA CTTTTCCT | TACGGTAGCAGAGACTTGGTCTC TTTTCATCACGTTCGGGTTGTC | 187 | 36 | ACCAGAAGAATTGCATAACTTTTCCTTAAATTCTGAATTACATTCTGACAT AAGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTA AACACAAAATACTGAAAGAAAGTGTCCCAGTTGGTACTGGAAATCAACTA GTGACCTTCCAGGGACAACCCGAACGTGATGAAAAG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_57 | 13 | 32912966 | 32913164 | ACACTGACGACATGGTTCTA CAAAAGAAAGTGTCCCAGTT GGT | TACGGTAGCAGAGACTTGGTCTT GGTGATTTCACTAGTACCTTGC | 199 | 39 | AAAGAAAGTGTCCCAGTTGGTACTGGAAATCAACTAGTGACCTTCCAGG GACAACCCGAACGTGATGAAAAGATCAAAGAACCTACTCTATTGGGTTTT CATACAGCTAGCGGGAAAAAAGTTAAAATTGCAAAGGAATCTTTGGACAA AGTGAAAAACCTTTTTGATGAAAAAGAGCAAGGTACTAGTGAAATCACCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_58 | 13 | 32913064 | 32913248 | ACACTGACGACATGGTTCTA CATCATACAGCTAGCGGGAA AAAAGT | TACGGTAGCAGAGACTTGGTCTT GATCTCAATGGTCTCACATGCT | 185 | 38 | TCATACAGCTAGCGGGAAAAAAGTTAAAATTGCAAAGGAATCTTTGGACA AAGTGAAAAACCTTTTTGATGAAAAAGAGCAAGGTACTAGTGAAATCACC AGTTTTAGCCATCAATGGGCAAAGACCCTAAAGTACAGAGAGGCCTGTA AAGACCTTGAATTAGCATGTGAGACCATTGAGATCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_59 | 13 | 32913185 | 32913382 | ACACTGACGACATGGTTCTA CAAAGACCCTAAAGTACAGA GAGGC | TACGGTAGCAGAGACTTGGTCTT GATGTTTTGAGATTTTCAGTTTGT CT | 198 | 37 | AAGACCCTAAAGTACAGAGAGGCCTGTAAAGACCTTGAATTAGCATGTG AGACCATTGAGATCACAGCTGCCCCAAAGTGTAAAGAAATGCAGAATTC TCTCAATAATGATAAAAACCTTGTTTCTATTGAGACTGTGGTGCCACCTA AGCTCTTAAGTGATAATTTATGTAGACAAACTGAAAATCTCAAAACATCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_60 | 13 | 32913301 | 32913486 | ACACTGACGACATGGTTCTA CACCTTGTTTCTATTGAGACT GTGGTG | TACGGTAGCAGAGACTTGGTCTT CAATGACTGAATAAGGGGACTG | 186 | 33 | CCTTGTTTCTATTGAGACTGTGGTGCCACCTAAGCTCTTAAGTGATAATT TATGTAGACAAACTGAAAATCTCAAAACATCAAAAAGTATCTTTTTGAAAG TTAAAGTACATGAAAATGTAGAAAAAGAAACAGCAAAAAGTCCTGCAACT TGTTACACAAATCAGTCCCCTTATTCAGTCATTGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_61 | 13 | 32913356 | 32913547 | ACACTGACGACATGGTTCTA CAAGACAAACTGAAAATCTC AAAACATCAAA | TACGGTAGCAGAGACTTGGTCTT GAAGTCTGACTCACAGAAGTTTT TC | 192 | 32 | AGACAAACTGAAAATCTCAAAACATCAAAAAGTATCTTTTTGAAAGTTAAA GTACATGAAAATGTAGAAAAAGAAACAGCAAAAAGTCCTGCAACTTGTTA CACAAATCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTA CACAAGTTGTAGTAGAAAAACTTCTGTGAGTCAGACTTCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_62 | 13 | 32913476 | 32913669 | ACACTGACGACATGGTTCTA CATCAGTCATTGAAAATTCA GCCTTAGC | TACGGTAGCAGAGACTTGGTCTT CAGCTATAGTACTGTTTGAATTAT TTTCAT | 194 | 31 | TCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAA ACTTCTGTGAGTCAGACTTCATTACTTGAAGCAAAAAAATGGCTTAGAGA AGGAATATTTGATGGTCAACCAGAAAGAATAAATACTGCAGATTATGTAG GAAATTATTTGTATGAAAATAATTCAAACAGTACTATAGCTGA | Assays designed by relax mode and have no off-target hits |

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| BRCA2 | BRCA2_63 | 13 | 32913566 | 32913759 | ACACTGACGACATGGTTCTACATGGCTTAGAGAAGGAATATTTGATGGT | TACGGTAGCAGAGACTTGGTCTACCTCATCAGAATGGTAGGAATAGC | 194 | 31 | TGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAAGAATAAATACTGCAGATTATGTAGGAAATTATTTGTATGAAAATAATTCAAACAGTACTATAGCTGAAAATGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCCTACCATTCTGATGAGGTTTCAAACAGTACTATAGCTGAAAATGACAAAAATCATCTCTCCGAAAAAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_64 | 13 | 32913649 | 32913831 | ACACTGACGACATGGTTCTACATTCAAACAGTACTATAGCTGAAAATGAC | TACGGTAGCAGAGACTTGGTCTTCAACATTCTTCAATACTGGCTCAA | 183 | 32 | AAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCCTACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGCCAGTATTGAAGAATGTTGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_65 | 13 | 32913735 | 32913933 | ACACTGACGACATGGTTCTACAGCTATTCCTACCATTCTGATGAGGT | TACGGTAGCAGAGACTTGGTCTACAAGTTCCTCAACGCAAATATC | 199 | 32 | GCTATTCCTACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAATAAACTTGATTCTGGTATTGAGCCAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAAAGATGCAAATGCATACCCACAAACTGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_66 | 13 | 32913854 | 32914036 | ACACTGACGACATGGTTCTACATCCAAAGTAATATCCAATGTAAAAGATGC | TACGGTAGCAGAGACTTGGTCTACTGGCTATCCTAAATGCAGGTG | 183 | 36 | TCCAAAGTAATATCCAATGTAAAAGATGCAAATGCATACCCACAAACTGTAAATGAAGATATTTGCGTTGAGGAACTTGTAAAATAAAAATGCAGCCATTAAATTGTCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCATTTAGGATAGCCAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_67 | 13 | 32913964 | 32914149 | ACACTGACGACATGGTTCTACATGCAGCCATTAAATTGTCCATATCT | TACGGTAGCAGAGACTTGGTCTTGGCAAATTTTTGATTTATTCTCGTTGTTT | 186 | 32 | TGCAGCCATTAAATTGTCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCATTTAGGATAGCCAGTGGTAAAATCGTTTGTGTTTCACATGAAACAATTAAAAAAGTGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGAAAACAACGAGAATAAATCAAAACAGACAGTTTCAGTAAAGTAATTAAGGAAAACAACGAGAATAAATCAAAAATTTGCCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_68 | 13 | 32914091 | 32914275 | ACACTGACGACATGGTTCTACAACAGACAGTTTCAGTAAAGTAATTAAGGA | TACGGTAGCAGAGACTTGGTCTTCTTCACTCTGAATGTCAGCAAA | 185 | 35 | AATTTGCCAAACGAAAATTATGGCAGGTTGTTACGAGGCATTGGATGATTCAGAGGATATTCTTCATAACTCTCTAGATAATGATGAATGTAGCACGCATTCACATAAGGTTTTTGCTGACATTCAGAGTGAAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_69 | 13 | 32914156 | 32914353 | ACACTGACGACATGGTTCTACAAATTATGGCAGGTTGTTACGAGG | TACGGTAGCAGAGACTTGGTCTGTTTCCAAACTAACATCACAAGGT | 198 | 34 | AATTATGGCAGGTTGTTACGAGGCATTGGATGATTCAGAGGATATTCTTCATAACTCTCTAGATAATGATGAATGTAGCACGCATTCACATAAGGTTTTTGCTGACATTCAGAGTGAAGAAATTTTACAACATAACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCACCTTGTGATGTTAGTTTGGAAAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_70 | 13 | 32914255 | 32914448 | ACACTGACGACATGGTTCTACATGCTGACATTCAGAGTGAAGAAA | TACGGTAGCAGAGACTTGGTCTCAGATTTTCCACTTGCTGTGCTAA | 194 | 34 | TGCTGACATTCAGAGTGAAGAAATTTTACAACATAACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCACCTTGTGATGTTAGTTTGGAAACTTCAGATATATGTAAATGTAGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGGAAAATC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_71 | 13 | 32914397 | 32914568 | ACACTGACGACATGGTTCTACAGTCTCATCTGCAAATACTTGTGGG | TACGGTAGCAGAGACTTGGTCTTGAGCTGGTCTGAATGTTCGTTA | 172 | 37 | GTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGGAAAATCTGTCCAGGTATCAGATGCTTCATTACAAAACGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCACGAACATTCAGACCAGCTCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_72 | 13 | 32914478 | 32914674 | ACACTGACGACATGGTTCTACAGCAAGACAAGTGTTTTCTGAAATAGAAG | TACGGTAGCAGAGACTTGGTCTGCTGTACTAAATCCAGAGAAAGCAGA | 197 | 35 | GCAAGACAAGTGTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCCAAAGTATTGTTTAAAAGTAAAATACTGCTATACGTACTCCAGAACATTTAATATCCCAAAAAGGCTTTTCATATAATGTGGTAAATTCATCTGCTTTCTCTGGATTTAGTACAGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_73 | 13 | 32914546 | 32914737 | ACACTGACGACATGGTTCTACATAACGAACATTCAGACCAGCTCA | TACGGTAGCAGAGACTTGGTCTTCCTCTAACACTCCCTTAACTTTGTG | 192 | 36 | TAACGAACATTCAGACCAGCTCACAAGAGAAGAAAATACTGCTATACGTACTCCAGAACATTTAATATCCCAAAAAGGCTTTTCATATAATGTGGTAAATTCATCTGCTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTTCCATTTTAGAAAGTTCCTTACACAAAGTTAAGGGAGTGTTAGAGGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_74 | 13 | 32914658 | 32914834 | ACACTGACGACATGGTTCTACATCTGGATTTAGTACAGCAAGTGGA | TACGGTAGCAGAGACTTGGTCTTGGGTTTCTCTTATCAACACGAGG | 177 | 36 | TCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTTCCATTTTAGAAAGTTCCTTACACAAAGTTAAGGGAGTGTTAGAGGAAGTTTAATTATCAAATAACTTAGCATAGTCTTCACTATTCACCTACGTCTAGACAAAATGTATCAAAAATACTTCCTCGTGTTGATAAGAGAAACCCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_75 | 13 | 32914749 | 32914934 | ACACTGACGACATGGTTCTACATCAGAACTGAGCATAGTCTTCACT | TACGGTAGCAGAGACTTGGTCTAGTGATTATTTTCTGAAGAACCACCTT | 186 | 33 | TCAGAACTGAGCATAGTCTTCACTATTCACCTACGTCTAGACAAAATGTATCAAAAATACTTCCTCGTGTTGATAAGAGAAACCCAGAGCACTGTGTAAACTCAGAAATGGAAAAAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_76 | 13 | 32914851 | 32915046 | ACACTGACGACATGGTTCTACACAGAAATGGAAAAAACCTGCAGTA | TACGGTAGCAGAGACTTGGTCTGCCTGTTCTTTTCCCAAAACATGAA | 196 | 32 | CAGAAATGGAAAAAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACTCTATTAAAGTTTCTCCATATCTCTCAATTTCAACAAGACAAACAACAGTTGGTATTAGGAACCAAAGTGTCGTGTCACTTGTTGAGAACATTCATGTTTTGGGAAAAGAACAGGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_77 | 13 | 32914958 | 32915151 | ACACTGACGACATGGTTCTACATCTCAATTTCAACAAGACAAACAACA | TACGGTAGCAGAGACTTGGTCTTCTGAATCTTTGGAGTAAGTAGAACA | 194 | 33 | TCTCAATTTCAACAAGACAAACAACAGTTGGTATTAGGAACCAAAGTGTCACTTGTTGAGAACATTCATGTTTTGGGAAAAGAACAGGCTTCACCTAAAAACGTAAAAATGGAAATTGGTAAAACTGAAACTTTTTCTGATGTTCCTGTGAAAAACAAATATAGAAGTTTGTTCTACTTACTCCAAAGATTCAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_78 | 13 | 32915045 | 32915243 | ACACTGACGACATGGTTCTACAGCTTCACCTAAAAACGTAAAAATGGAA | TACGGTAGCAGAGACTTGGTCTGTGTGGCATGACTTGGCAGTTTA | 199 | 34 | GCTTCACCTAAAAACGTAAAAATGGAAATTGGTAAAACTGAAACTTTTTCTGATGTTCCTGTGAAAACAAATATAGAAGTTTGTTCTACTTACTCCAAAGATTCAGAAAACTACTTTGAAACAGAAGCAGTAGAAATTGCTAAAGCTTTTATGGAAGATGATGAACTGACAGATTCTAAACTGCCAAGTCATGCCACACAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_79 | 13 | 32915188 | 32915372 | ACACTGACGACATGGTTCTACAAGCTTTTATGGAAGATGATGAACTGA | TACGGTAGCAGAGACTTGGTCTTAGTGATTGGCAACACGAAAGGT | 185 | 38 | AGCTTTTATGGAAGATGATGAACTGACAGATTCTAAACTGCCAAGTCATGCCACACATTCTCTTTTTACATGTCCCGAAAATGAGGAAATGGTTTTGTCAAATTCAAGAATTGGAAAAAGAAGAGGAGAGCCCCTTATCTTAGTGGGTAAGTGTTCATTTTTACCTTTCGTGTTGCCAATCACTA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_80 | 13 | 32918559 | 32918755 | ACACTGACGACATGGTTCTACACACTATTTGTTGTAAGTATTTTTGTTTAACATTT | TACGGTAGCAGAGACTTGGTCTGCTTGATTTTCTATTATCCTGTCAAATTCAT | 197 | 23 | CACTATTTGTTGTAAGTATTTTTGTTTAACATTTAAAGAGTCAATACTTTAGCTTTAAAAAAATGGTCTATAGACTTTTGAGAAATAAAACTGATATTATTTGCCTTAAAAACATATATGAAATATTTCTTTTTAGGAGAACCCTCAATCAAAAGAAACTTATTAAATGAATTTGACAGGATAATAGAAAATCAAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_81 | 13 | 32918683 | 32918853 | ACACTGACGACATGGTTCTACAATTTCTTTTTAGGAGAACCCTCAATCAA | TACGGTAGCAGAGACTTGGTCTGTCAGAATATTATATACCATACCTATAGAGGGAGA | 171 | 29 | ATTTCTTTTTAGGAGAACCCTCAATCAAAAGAAACTTATTAAATGAATTTGACAGGATAATAGAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT | Assays designed by relax mode and have no off-target hits |

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| | | | | | | | | | CCAGATGGTAAAATTAGCTTTTTATTTATATCTGTTCTCCCTCTATAGGTA TGGTATATAATAttctgac | |
| BRCA2 | BRCA2_83 | 13 | 32920895 | 32921044 | ACACTGACGACATGGTTCTA CAGTATTTACAGTAACATGG ATATTCTCTTAGATTT | TACGGTAGCAGAGACTTGGTCTA CATGTCTTACCGAAAGGGTACA | 150 | 31 | GTATTTACAGTAACATGGATATTCTCTTAGATTTTAACTAATATGTAATATA AAATAATTGTTTCCTAGGCACAATAAAAGATCGAAGATTGTTTATGCATCA TGTTTCTTTAGAGCCGATTACCTGTGTACCCTTTCGGTAAGACATGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_127 | 13 | 32920953 | 32921102 | ACACTGACGACATGGTTCTA CATTGTTTCCTAGGCACAAT AAAAGA | TACGGTAGCAGAGACTTGGTCTT GTTCATTTATAAAAACGAGACTTT TC | 150 | 31 | TTGTTTCCTAGGCACAATAAAAGATCGAAGATTGTTTATGCATCATGTTTC TTTAGAGCCGATTACCTGTGTACCCTTTCGGTAAGACATGTTTAAATTTTT CTAAATTCTAATACAGTATGAGAAAAGTCTCGTTTTTATAAATGAACA | |
| BRCA2 | BRCA2_85 | 13 | 32928912 | 32929110 | ACACTGACGACATGGTTCTA CACAAATGAGGGTCTGCAAC AAAGG | TACGGTAGCAGAGACTTGGTCTT GCTTGAAGATTTTTCCAAAGTCA G | 199 | 35 | CAAATGAGGGTCTGCAACAAAGGCATATTCCTAAATATTTATATGTGTAC TAGTCAATAAACTTATATATTTTCTCCCCATTGCAGCACAACTAAGGAAC GTCAAGAGATACAGAATCCAAATTTTACCGCACCTGGTCAAGAATTTCTG TCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_86 | 13 | 32928997 | 32929195 | ACACTGACGACATGGTTCTA CAGCACAACTAAGGAACGTC AAGAG | TACGGTAGCAGAGACTTGGTCTG GTCTGCCTGTAGTAATCAAGTG | 199 | 36 | GCACAACTAAGGAACGTCAAGAGATACAGAATCCAAATTTTACCGCACC TGGTCAAGAATTTCTGTCTAAATCTCATTTGTATGAACATCTGACTTTGGA AAAATCTTCAAGCAATTTAGCAGTTTCAGGACATCCATTTTATCAAGTTTC TGCTACAAGAAATGAAAAAATGAGACACTTGATTACTACAGGCAGACC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_87 | 13 | 32929113 | 32929288 | ACACTGACGACATGGTTCTA CATTAGCAGTTTCAGGACAT CCATT | TACGGTAGCAGAGACTTGGTCTT GTCTGTTTTCCTCCAAGTTAATAT TCC | 176 | 35 | TTAGCAGTTTCAGGACATCCATTTTATCAAGTTTCTGCTACAAGAAATGA AAAAATGAGACACTTGATTACTACAGGCAGACCAACCAAAGTCTTTGTTC CACCTTTTAAAACTAAATCACATTTTCACAGAGTTGAACAGTGTGTTAGG AATATTAACTTGGAGGAAAACAGACA | |
| BRCA2 | BRCA2_88 | 13 | 32929181 | 32929377 | ACACTGACGACATGGTTCTA CATACTACAGGCAGACCAAC CAAAG | TACGGTAGCAGAGACTTGGTCTT GGAGTTGTTTTTGTTAAACTGATG A | 197 | 34 | TACTACAGGCAGACCAACCAAAGTCTTTGTTCCACCTTTTAAAACTAAAT CACATTTTCACAGAGTTGAACAGTGTGTTAGGAATATTAACTTGGAGGAA AACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAA TAAGATTAATGACAATGAGATTCATCAGTTTAACAAAAACAACTCCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_89 | 13 | 32929315 | 32929467 | ACACTGACGACATGGTTCTA CACTGATGATAGTAAAAATAA GATTAATGACAATGAG | TACGGTAGCAGAGACTTGGTCTA CTGAAAGGCAAAAATTCATCACA CA | 153 | 31 | CTGATGATAGTAAAAATAAGATTAATGACAATGAGATTCATCAGTTTAACA AAAACAACTCCAATCAAGCAGTAGCTGTAACTTTCACAAAGTGTGAAGAA GAACCTTTAGGTATTGTATGACAATTTGTGTGATGAATTTTTGCCTTTCAG T | |
| BRCA2 | BRCA2_90 | 13 | 32930503 | 32930690 | ACACTGACGACATGGTTCTA CAGGCCAGGGGTTGTGCTTT TTA | TACGGTAGCAGAGACTTGGTCTT TCGAGGCAGAGTGGATGTTTTT | 188 | 37 | ggccAGGGGTTGTGCTTTTTAAATTTCAATTTTATTTTTGCTAAGTATTTATT CTTTGATAGATTTAATTACAAGTCTTCAGAATGCCAGAGATATACAGGAT ATGCGAATTAAGAAGAAACAAAGGCAACGCGTCTTTCCACAGCCAGGCA GTCTGTATCTTGCAAAAACATCCACTCTGCCTCGAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_91 | 13 | 32930607 | 32930790 | ACACTGACGACATGGTTCTA CATGCGAATTAAGAAGAAAC AAAGGC | TACGGTAGCAGAGACTTGGTCTA CACTCTGTCATAAAAGCCATCAG T | 184 | 45 | TGCGAATTAAGAAGAAACAAAGGCAACGCGTCTTTCCACAGCCAGGCAG TCTGTATCTTGCAAAAACATCCACTCTGCCTCGAATCTCTCTGAAAGCAG CAGTAGGAGGCCAAGTTCCCTCTGCGTGTTCTCATAAACAGGTATGTGT TTGTCTACAATACTGATGGCTTTTATGACAGAGTGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_92 | 13 | 32931809 | 32932007 | ACACTGACGACATGGTTCTA CATTGTTTTTATTGTGTGATA CATGTTTACTTT | TACGGTAGCAGAGACTTGGTCTA GCCAACTGTATTCCTTTTCCAGT | 199 | 30 | TTGTTTTTATTGTGTGATACATGTTTACTTTAAATTGTTTTTCTTTTTTGTG TGTGTTTATTTTGTGTAGCTGTATACGTATGGCGTTTCTAAACATTGCATA AAAATTAACAGCAAAAATGCAGAGTCTTTTCAGTTTCACACTGAAGATTAT TTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGCT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_93 | 13 | 32931907 | 32932099 | ACACTGACGACATGGTTCTA CAGCATAAAAATTAACAGCA AAAATGCAG | TACGGTAGCAGAGACTTGGTCTA AAGTTAACACACAATCTTTTTGCA TAG | 193 | 36 | GCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTCAGTTTCACACTGAA GATTATTTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGC TGATGGTGGATGGCTCATACCCTCCAATGATGGAAAGGCTGGAAAAGAA GAATTTTATAGGTACTCTATGCAAAAAGATTGTGTGTTAACTTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_94 | 13 | 32936578 | 32936771 | ACACTGACGACATGGTTCTA CATGTACAGAGAATAGTTGT AGTTGTTGA | TACGGTAGCAGAGACTTGGTCTA GGAAAGGCACATTCCATAGCTG | 194 | 36 | TGTACAGAGAATAGTTGTAGTTGTTGAATTCAGTATCATCCTATGTGGTT TTTATGATAATATTCTACTTTTATTTGTTCAGGGCTCTGTGTGACACTCCA GGTGTGGATCCAAAGCTTATTTCTAGAATTTGGGTTTATAATCACTATAG ATGGATCATATGGAAACTGGCAGCTATGGAATGTGCCTTTCCT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_95 | 13 | 32936661 | 32936831 | ACACTGACGACATGGTTCTA CAGCTCTGTGTGACACTCCA GGT | TACGGTAGCAGAGACTTGGTCTC CTGTATTTTAGTTGAAGAAGCAC CC | 171 | 41 | GCTCTGTGTGACACTCCAGGTGTGGATCCAAAGCTTATTTCTAGAATTTG GGTTTATAATCACTATAGATGGATCATATGGAAACTGGCAGCTATGGAAT GTGCCTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCCAGAAAGGGT GCTTCTTCAACTAAAATACAGG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_96 | 13 | 32936738 | 32936933 | ACACTGACGACATGGTTCTA CAATGGAAACTGGCAGCTAT GGAAT | TACGGTAGCAGAGACTTGGTCTG ACAACTGGCTTGTGCAACATTT | 196 | 40 | ATGGAAACTGGCAGCTATGGAATGTGCCTTTCCTAAGGAATTTGCTAATA GATGCCTAAGCCCAGAAAGGGTGCTTCTTCAACTAAAATACAGGCAAGT TTAAAGCATTACATTACGTAATCATATACGGCAGTATGGTTAAGGTTTCT GTGTAGTCTGTGACTTCCATGTCAAAATGTTGCACAAGCCAGTTGTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_97 | 13 | 32937263 | 32937433 | ACACTGACGACATGGTTCTA CATGGAATTCTAGAGTCACA CTTCCTAA | TACGGTAGCAGAGACTTGGTCTT GCGCTCAATGAAATTATGTCAGA AAC | 171 | 35 | TGGAAATTCTAGAGTCACACTTCCTAAAATATGCATTTTTGTTTTCACTTTT AGATATGATACGGAAATTGATAGAAGCAGAAGATCGGCTATAAAAAAGAT AATGGAAAGGGATGACACAGCTGCAAAAACACTTGTTCTCTGTGTTTCTG ACATAATTTCATTGAGCGCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_98 | 13 | 32937366 | 32937563 | ACACTGACGACATGGTTCTA CATGGAAAGGGATGACACAG C | TACGGTAGCAGAGACTTGGTCTT CTTTAAGACAGCTAAGAGGGGAG | 198 | 40 | TGGAAAGGGATGACACAGCTGCAAAAACACTTGTTCTCTGTGTTTCTGA CATAATTTCATTGAGCGCAAATATATCTGAAACTTCTAGCAATAAAACTAG TAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGG TATGCTGTTAAGGCCCAGTTAGATCCTCCCCTCTTAGCTGTCTTAAAGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_99 | 13 | 32937465 | 32937648 | ACACTGACGACATGGTTCTA CAGTAGTGCAGATACCCAAA AAGTGG | TACGGTAGCAGAGACTTGGTCTG CTTCAAGAGGTGTACAGGCATC | 184 | 47 | GTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTG GTATGCTGTTAAGGCCCAGTTAGATCCTCCCCTCTTAGCTGTCTTAAAGA ATGGCAGACTGACAGTTGGTCAGAAGATTATTCTTCATGGAGCAGAACT GGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_100 | 13 | 32937594 | 32937785 | ACACTGACGACATGGTTCTA CATTCTTCATGGAGCAGAAC TGGTG | TACGGTAGCAGAGACTTGGTCTT CAGTACATCTAAGAAATTGAGCA TCC | 192 | 35 | TTCTTCATGGAGCAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCT TGAAGCCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTTGG TAAAAATCAGTCATTGATTCAGTTAAATTCTAGAAGTTTTACATTTAAATTT TAAATGCTTACTAAGGATGCTCAATTTCTTAGATGTACTGA | |
| BRCA2 | BRCA2_101 | 13 | 32944423 | 32944616 | ACACTGACGACATGGTTCTA CATTTTTAAAGTGAATATTTT TAAGGCAGTTCT | TACGGTAGCAGAGACTTGGTCTC AGAGGAAAAGGTCTAGGGTCAG | 194 | 32 | TTTTTAAAGTGAATATTTTTAAGGCAGTTCTAGAAGAATGAAAACTCTTAT GATATCTGTAATAGAATTGAATACATATTTAACTACTAAATCAATATATTTA | Assays designed by relax mode and have no off-target hits |

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| | | | | | | | | | TTAATTTGTCCAGATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAACTTGGATTCTTTCCTGACCCTAGACCTTTTCCTCTG | |
| BRCA2 | BRCA2_102 | 13 | 32944558 | 32944739 | ACACTGACGACATGGTTCTACAGGCCTGCTCGCTGGTAT | TACGGTAGCAGAGACTTGGTCTATCAAAAGAAAGAAATATATGGTAAGTTTCAAG | 182 | 39 | GGCCTGCTCGCTGGTATACCAAACTTGGATTCTTTCCTGACCCTAGACCTTTTCCTCTGCCCTTATCATCGCTTTTCAGTGATGGAGGAAATGTTGGTTGTGTTGATGTAATTATTCAAAGAGCATACCCTATACAGGTATGATGTATTCTTGAAACTTACCATATATTTCTTTCTTTTGAT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_103 | 13 | 32945018 | 32945192 | ACACTGACGACATGGTTCTACACTGTGCCTGGCCTGATACAATTA | TACGGTAGCAGAGACTTGGTCTCTAGTCTCTTTTGTTGGGCCTCC | 175 | 38 | ctgtgcctggccTGATACAATTAACTTGAATGTTATATATGTGACTTTTTTGGTGTGTGTAACACATTATTACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTCGCAATGAAAGAGAGGAAGAAAAGGAAGCAGCAAAATATGTGGAGGCCCAACAAAAGAGACTAG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_104 | 13 | 32945088 | 32945279 | ACACTGACGACATGGTTCTACATACAGTGGATGGAGAAGACATCA | TACGGTAGCAGAGACTTGGTCTTCATATTAGAAATAACAATGTGTACCATATAACT | 192 | 34 | TACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTCGCAATGAAAGAGAGGAAGAAAAGGAAGCAGCAAAATATGTGGAGGCCCAACAAAAGAGACTAGAAGCCTTATTCACTAAAATTCAGGAGGAATTTGAAGAACATGAAGGTAAAATTAGTTATATGGTACACATTGTTATTTCTAATATGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_105 | 13 | 32950735 | 32950927 | ACACTGACGACATGGTTCTACATGCTTGGTTCTTTAGTTTTAGTTGCT | TACGGTAGCAGAGACTTGGTCTTCAAGGTAAGCTGGGTCTGC | 193 | 37 | TGCTTGGTTCTTTAGTTTTAGTTGCTTTTGAATTTACAGTTTAGTGAATTAATAATCCTTTTGTTTTCTTAGAAAACACAACAAAACCATATTTACCATCACGTGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCCAGCTTACCTTGA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_106 | 13 | 32950838 | 32951010 | ACACTGACGACATGGTTCTACATGCACTAACAAGACAGCAAGTTC | TACGGTAGCAGAGACTTGGTCTCCTGTGATGGCCAGAGAGTCTAA | 173 | 45 | TGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCCAGCTTACCTTGAAGTAAGAGGACATATAATGAGGCTTGATGATTATTCAAGGTGAGAAGCTGTTTTAGACTCTCTGGCCATCACAGG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_107 | 13 | 32953398 | 32953576 | ACACTGACGACATGGTTCTACAAGATGGAACTTTTTTGTTCTGATTGC | TACGGTAGCAGAGACTTGGTCTTTCCTTTTGTTCAGCAGATTCCA | 179 | 36 | AGATGGAACTTTTTTGTTCTGATTGCTTTTTATTCCAATATCTTAAATGGTCACAGGGTTATTTCAGTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAACAAGCTCAGATCCAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAGGAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_108 | 13 | 32953496 | 32953694 | ACACTGACGACATGGTTCTACAAGGCAAATGTTGAATGATAAGAAACA | TACGGTAGCAGAGACTTGGTCTAAGTTAATAAAACTGATAAAAACAAAGCATTTAC | 199 | 35 | AGGCAAATGTTGAATGATAAGAAACAAGCTCAGATCCAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAAGAAAAAGATTCAGGTAAGTATGTAAATGCTTTGTTTTTATCAGTTTTATTAACTT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_109 | 13 | 32953847 | 32954025 | ACACTGACGACATGGTTCTACACACTTCTTCCATTGCATCTTTCTCA | TACGGTAGCAGAGACTTGGTCTTTTGTCGCTGCTAACTGTATGTT | 179 | 34 | CACTTCTTCCATTGCATCTTTCTCATCTTTCTCCAAACAGTTATACTGAGTATTTGGCGTCCATCATCAGATTTATATTCTCTGTTAACAGAAGGAAAGAGATACAGAATTTATCATCTTGCAACTTCAAAATCTAAAAGTAAATCTGAAAGAGCAGCTAACATACAGTTAGCAGCGACAAA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_110 | 13 | 32953901 | 32954099 | ACACTGACGACATGGTTCTACATGGCGTCCATCATCAGATTTATATTC | TACGGTAGCAGAGACTTGGTCTACTAACAAGCACTTATCAAAACTGAAA | 199 | 33 | TGGCGTCCATCATCAGATTTATATTCTCTGTTAACAGAAGGAAAGAGATACAGAATTTATCATCTTGCAACTTCAAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAAAAACTCAGTATCAACAACTACCGGTACAAACCTTTCATTGTAATTTTTCAGTTTTGATAAGTGCTTGTTA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_111 | 13 | 32954047 | 32954235 | ACACTGACGACATGGTTCTACAACCGGTACAAACCTTTCATTGT | TACGGTAGCAGAGACTTGGTCTGAACAAGATGGCTGAAAGTCTGG | 189 | 35 | ACCGGTACAAACCTTTCATTGTAATTTTTCAGTTTTGATAAGTGCTTGTTAGTTTATGGAATCTCCATATGTTGAATTTTTGTTTTGTTTTCTGTAGGTTTCAGATGAAATTTTATTTCAGATTTACCAGCCACGGGAGCCCCTTCACTTCAGCAAATTTTTAGATCCAGACTTTCAGCCATCTTGTTC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_112 | 13 | 32954171 | 32954369 | ACACTGACGACATGGTTCTACATACCAGCCACGGGAGCC | TACGGTAGCAGAGACTTGGTCTTGGTAGCTCCAACTAATCATAAGAGA | 199 | 35 | TACCAGCCACGGGAGCCCCTTCACTTCAGCAAATTTTTAGATCCAGACTTTCAGCCATCTTGTTCTGAGGTGGACCTAATAGGATTTGTCGTTTCTGTTGTGAAAAAAACAGGTAATGCACAATATAGTTAATTTTTTTTATTGATTCTTTTAAAAAACATTGTCTTTTAAAATCTCTTATGATTAGTTGGAGCTACCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_Intron_24__region_1__1 | 13 | 32955429 | 32955627 | ACACTGACGACATGGTTCTACAGGGGAGGGAGATTACAAACAAAG | TACGGTAGCAGAGACTTGGTCTACCTCACTCCCTCAATTCCTTCA | 199 | 40 | ggggagggagattacaaacaaagaaataagtaatatacatgtgtatagttttttagtgctcagaaaaaaaattaagtgggtaaggggggtaatgtcagagaagagagagggatgtaatttagattgagaggtgaggagagagacctccctggaaagctgacatttgagtgaagcttgaaggaattgagggagtgaggt | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__2 | 13 | 32955521 | 32955716 | ACACTGACGACATGGTTCTACATGTCAGAGAAGAGAGAGGGATGT | TACGGTAGCAGAGACTTGGTCTCAATGCTTCACGGCACACTAGG | 196 | 49 | tgtcagagaagagagagggatgtaattttagattgagaggtgaggagagagacctccctggaaagctgacatttgagtgaagcttgaaggaattgagggagtgaggtgaggcatgtggccatctggggaaagctttccaggcaattacaaaggccgcagtacagcaggatcatgcctagtgtgccgtgaagcattg | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__3 | 13 | 32955600 | 32955779 | ACACTGACGACATGGTTCTACAAAGCTTGAAGGAATTGAGGGAGT | TACGGTAGCAGAGACTTGGTCTCACACGACCTGGCTCTTCAC | 180 | 53 | aagcttgaaggaattgagggagtgaggtgaggcatgtggccatctggggaaagctttccaggcaattacaaaggccgcagtacagcaggatcatgcctagtgtgccgtgaagcattggcagagaccagagagtgagaagtaacatccagggacagaggcagtgaagagccaggtcgtgtg | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__4 | 13 | 32955731 | 32955909 | ACACTGACGACATGGTTCTACAGTGAGAAGTAACATCCAGGGACA | TACGGTAGCAGAGACTTGGTCTCCCCTACAGCCTATTCTCAACAC | 179 | 51 | gtgagaagtaacatccagggacagaggcagtgaagagccaggtcgtgtgggggtccttgtgtggactgtaacttcctgtgatgacaggaagtcacaggaaaattccaggtagagggacactgtctgacaggttttcacagaatcattcaggccactgtgttgagacaggaaaattccaggtagagggacactgtctgacaggttttcacagaatcattcaggccactgtgttgagaatggcttgaggggcacaagagtacaaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaaaataggaattgccacttagaaggaaagactgcaagaaaagca | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__5 | 13 | 32955824 | 32956006 | ACACTGACGACATGGTTCTACAACAGGAAAATTCCAGGTAGAGGG | TACGGTAGCAGAGACTTGGTCTGACTGCTTCTCACCACTTCCATT | 183 | 45 | aataggctgtaggggggcacaagagtacaaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaaaataggaattgccacttagaaggaaagactgcaagaaaagcagtggtgagaagcagtcagattcttgttgtattttgaaggtaggggggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaaggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaaagcaagtatgtggggaagttcaggagctcagttttagacagttaagttttagatgcttattaggcatctaagtagaaatgtctacttgatggttacataggaatctgttcagaggaatggctgg | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__6 | 13 | 32955922 | 32956107 | ACACTGACGACATGGTTCTACAAAACAAGCCATTTGGAGGCTCTT | TACGGTAGCAGAGACTTGGTCTTGCTTTTCTTGCAGTCTTTCCTT | 186 | 42 | aaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaagtggtgagaagcagtcagattcttgttgtattttgaaggtaggggggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagca | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_1__7 | 13 | 32956034 | 32956227 | ACACTGACGACATGGTTCTACAGGGACGGTGCAGGATGG | TACGGTAGCAGAGACTTGGTCTCCAGCCATTCCTCTGAACAGATT | 194 | 42 | gggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaagcaagtatgtggggaagttcaggagctcagttttagacagttaagttttagatgcttattaggcatctaagtagaaatgtctacttgatggttacataggaatctgttcagaggaatggctgg | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_2__1 | 13 | 32958725 | 32958923 | ACACTGACGACATGGTTCTACAAAGTGAGGAGGCCTAGATGTCAG | TACGGTAGCAGAGACTTGGTCTTCTGGTCCAAGACTCTGTTTTCC | 199 | 43 | AAGTGAGGAGGCCTAGATGTCAGAGGAGTCCGGCTAAACCACTGCAGAACTGCTGCCTAATTCACAGCAACCATGAGTAAAAATGCTGATGATCATCAGGGTCAAGGATAGTCTGGAGCAGTTAAGATGTTACTTTACATGGGAGGTATCAATTAAAGATGATGAAATGCCTGATTTGGAAAACAGAGTCTTGGACCAGA | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_2__2 | 13 | 32958830 | 32959024 | ACACTGACGACATGGTTCTACAGATAGTCTGGAGCAGTTAAGATGT | TACGGTAGCAGAGACTTGGTCTAGTTCTCCAGCACTTCCTCATTC | 195 | 41 | GATAGTCTGGAGCAGTTAAGATGTTACTTTACATGGGAGGTATCAATTAAAGATGATGAAATGCCTGATTTGGAAAACAGAGTCTTGGACCAGATTGGG | Two primers sits in the repeat region |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | TTTCTAGACTAAATACAGTGTGGGAATACACAATACACAACCTACTAGCC<br>TATGTGAAACACCCGAAAGGCCAGAATGAGGAAGTGCTGGAGAACT | |
| BRCA2 | BRCA2_Intron_24__region_2__3 | 13 | 32958974 | 32959172 | ACACTGACGACATGGTTCTACATAGCCTATGTGAAACACCCGAAA | TACGGTAGCAGAGACTTGGTCTGCAAATGTTCTCTACCTTGTCCA | 199 | 47 | TAGCCTATGTGAAACACCCGAAAGGCCAGAATGAGGAAGTGCTGGAGA<br>ACTTGAAAGAAGCTGAAGACTTAATCCAGAAAGAAGATGCCAATCAGATT<br>TGAGAAGCCTGGTAACCTGGGGCAACTTTGCCTGGGTGTATTACCACAT<br>GGGCAGACTGGCAGAAACCCAGACTTACCTGGACAAGGTAGAGAACAT<br>TTGC | |
| BRCA2 | BRCA2_Intron_24__region_2__4 | 13 | 32959058 | 32959234 | ACACTGACGACATGGTTCTACAATGCCAATCAGATTTGAGAAGCC | TACGGTAGCAGAGACTTGGTCTTCTTCCTCACAGTCCATCTCTGG | 177 | 47 | ATGCCAATCAGATTTGAGAAGCCTGGTAACCTGGGGCAACTTTGCCTGG<br>GTGTATTACCACATGGGCAGACTGGCAGAAACCCAGACTTACCTGGACA<br>AGGTAGAGAACATTTGCAAGAAGTTTTCAAGTCCTTTCTGTCACAGAATG<br>GAATGTCCAGAGATGGACTGTGAGGAAGA | |
| BRCA2 | BRCA2_Intron_24__region_2__5 | 13 | 32959147 | 32959333 | ACACTGACGACATGGTTCTACAACCTGGACAAGGTAGAGAACATT | TACGGTAGCAGAGACTTGGTCTGTGTTGAGTTCAGGGTTTTCAGC | 187 | 48 | ACCTGGACAAGGTAGAGAACATTTGCAAGAAGTTTTCAAGTCCTTTCTGT<br>CACAGAATGGAATGTCCAGAGATGGACTGTGAGGAAGAACGGGCCTTG<br>CTGGAATGTGGAGGGAAGAATTATGAACAGGCCAAGGCCTGCTTTGAAA<br>AGGATCTGGCAGTGGCTGCTGAAAACCCTGAACTCAACAC | |
| BRCA2 | BRCA2_Intron_24__region_2__6 | 13 | 32959205 | 32959401 | ACACTGACGACATGGTTCTACAGGAATGTCCAGAGATGGACTGTG | TACGGTAGCAGAGACTTGGTCTAAAATGACTTGTGATCCCCCGTT | 197 | 50 | GGAATGTCCAGAGATGGACTGTGAGGAAGAACGGGCCTTGCTGGAATG<br>TGGAGGGAAGAATTATGAACAGGCCAAGGCCTGCTTTGAAAAGGATCTG<br>GCAGTGGCTGCTGAAAACCCTGAACTCAACACTGGGTATGAAATCACCG<br>CCTGTCGCCTGGATGGCTTTAAATTAGCAACGGGGGATCACAAGTCATT<br>TT | |
| BRCA2 | BRCA2_Intron_24__region_2__7 | 13 | 32959311 | 32959504 | ACACTGACGACATGGTTCTACAGCTGAAAACCCTGAACTCAACAC | TACGGTAGCAGAGACTTGGTCTCCTTCAGCTTCCTGTCCTTCATC | 194 | 47 | GCTGAAAACCCTGAACTCAACACTGGGTATGAAATCACCGCCTGTCGCC<br>TGGATGGCTTTAAATTAGCAACGGGGGATCACAAGTCATTTTCTTTGCCT<br>ACCCTAAGGCAGGCTGTCAGGCTAAATGTAGATGATAGATATAGTAAGG<br>TTCTTCTTGCCCTGAAGCTTTGGGATGAAGGACAGGAAGCTGAAGG | |
| BRCA2 | BRCA2_Intron_24__region_3__1 | 13 | 32964498 | 32964682 | ACACTGACGACATGGTTCTACAGCGGCTCGCAAGGCTA | TACGGTAGCAGAGACTTGGTCTACAAAGAAGATTTTTAAAGGTAGGAAGCA | 185 | 32 | gcggctcgcaaggctaggagtttgggacaagtctgggcaacagtgagattctgtctctataaacataaaaaCTAAATTTAAAAAAAAAACTACTTTAAAACATAATAATAAAACAAACTGTACAAGTTCATATTCCTGATGCATGATAACATTTAATgcttcctacctttaaaaatcttctttgt | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_Intron_24__region_3__2 | 13 | 32964614 | 32964772 | ACACTGACGACATGGTTCTACAACTGTACAAGTTCATATTCCTGATGC | TACGGTAGCAGAGACTTGGTCTAAGCATCTGACTAGGGAGGTAAT | 159 | 35 | ACTGTACAAGTTCATATTCCTGATGCATGATAACATTTAATgcttcctaccttaaaaatcttctttgttttgcatagatgctcttttgttctccccctcttgatgaatttgtcctattcattattcagctcaagtattacctccctagtcagatgcttacagtctgggttcccctagtcagatgctt | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__3 | 13 | 32964707 | 32964900 | ACACTGACGACATGGTTCTACACCCCCTCTTGATGAATTTGTCCT | TACGGTAGCAGAGACTTGGTCTACTGAGGCTAGTAGGTGGCTTAT | 194 | 44 | cccccttgatgaatttgtcctattcattattcagctcaagtattacctccctagtcagatgcttacagtctgggttagatcctcctcctccagcttttgaagcattttgttggtttggctgtttcagcacttgtcacatggtccatgatcctactctgtacacttctgaataagccacctactagcctcagt | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__4 | 13 | 32964809 | 32965000 | ACACTGACGACATGGTTCTACAAAGCATTTTGTTGGTTTGGCTGT | TACGGTAGCAGAGACTTGGTCTCCTGGAGTTTTCAACAACTGACC | 192 | 44 | aagcattttgttggtttggctgtttcagcacttgtcacatggtccatgatcctacctgtacacttctgaataagccacctactagcctcagtaatacaatgatctcttcaaggacagggactctgtttGGATTTCTACTTCCACTTCTGACATAATGGGTTGAAGCAGGGGTCAGTTGTTGAAAACTCCAGG | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__5 | 13 | 32964908 | 32965094 | ACACTGACGACATGGTTCTACATGATCTCTTCAAGGACAGGGACT | TACGGTAGCAGAGACTTGGTCTTAACCTCTCTGAGCTCCAGTTTC | 187 | 44 | tgatctcttcaaggacagggactctgtttGGATTTCTACTTCCACTTCTGACATAATGGGTTGAAGCAGGGGTCAGTTGTTGAAAACTCCAGGTatgcagcatctcatacggtcctcatagtcacactgttcatttgctattatcatcccactttacagatggggaaactggagctcagagaggtta | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__6 | 13 | 32965017 | 32965207 | ACACTGACGACATGGTTCTACACGGTCCTCATAGTCACACTGTTC | TACGGTAGCAGAGACTTGGTCTTGAGTTTGCTTTTGTTTTGTCAGC | 191 | 40 | cggtcctcatagtcacactgttcatttgctattatcatcccactttacagatggggaaactggagctcagagaggttaagtagcctgctcagggtcacaatgctataaattgatttgaacttatactttcaggccctaaagctcttaggttctttcttatacttcatgctgACAAAACAAAAGCAAACTCA | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__7 | 13 | 32965060 | 32965244 | ACACTGACGACATGGTTCTACATTTACAGATGGGGAAACTGGAGC | TACGGTAGCAGAGACTTGGTCTTACAGATGTCCCTGTTTTAAGCC | 185 | 39 | tttacagatggggaaactggagctcagagaggttaagtagcctgctcagggtcacaatgctataaattgattgaacttatactttcaggccctaaagctcttaggttctttcttatacttcatgctgACAAAACAAAAGCAAACTCAACATTTGAGAGTTGGGCTTAAAACAGGGACATCTGTAtgctgACAAAACAAAAGCAAACTCAACATTTGAGAGTTGGGCTTAAAACAG | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__8 | 13 | 32965183 | 32965359 | ACACTGACGACATGGTTCTACAtgctgACAAAACAAAAGCAAACT | TACGGTAGCAGAGACTTGGTCTgaaACAGGCTTTCCCCAAAACAA | 177 | 34 | GGACATCTGTATTTTTAATCTAATGCTTTGTTACTGTATTACAGAAACACTGTGATATATAATGAGTTAATTAAACGAGAACCTTTCTTAGGTTGGGAAAGATTTGTTTTGGGGAAAGCCTGTttc | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__9 | 13 | 32965220 | 32965418 | ACACTGACGACATGGTTCTACATGGGCTTAAAACAGGGACATCTG | TACGGTAGCAGAGACTTGGTCTGCTGTTCCTAAGGGCATTTTCTA | 199 | 36 | TGGGCTTAAAACAGGGACATCTGTATTTTTAATCTAATGCTTTGTTACTGTATTACAGAAACACTGTGATATATAATGAGTTAATTAAACGAGAACCTTTCTTAGGTTGGGAAAGATTTGTTTTGGGGAAAGCCTGTttccctgggaaacagacttacagatttcatgtaggagattagaaaatgcccttaggaacagc | One primer sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__10 | 13 | 32965331 | 32965527 | ACACTGACGACATGGTTCTACAAAAGATTTGTTTTGGGGAAAGCC | TACGGTAGCAGAGACTTGGTCTCAGGCTAGCAAGACTCTGAAGG | 197 | 47 | AAAGATTTGTTTTGGGGAAAGCCTGTTtccctgggaaacagacttacagatttcatgtaggagattagaaaatgcccttaggaacagcacttgtgaggaagcaaatgcagcaggattgggcagaagaagaagaaaggttcagttagtcccacagggacttctggagctgggtggcccttcagagtcttgctagcctgcagcaggattgggcagaagaagaagaaaggttcagttagtcccacagggacttctggagctgggtggcccttcagagtcttgctagcctgaggcaagagccagtccttgcatactggctcctccagggaggggcatagccttaagcaagacaatgcctttcgacagagggcaagtccaggagggaactcagagcagagggcaagtccaggagggaactcagaggtgagttgtcaatagctagctctccccagaagctggagcatcacatgccttggtcctgaaggggatctgcacccgcaccatggcatccacTCCAGctggaggatcacatgccttggtcctgaaggggatctgcacccgcaccatggcatccacTCCAGGTG | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__11 | 13 | 32965437 | 32965630 | ACACTGACGACATGGTTCTACAGCAGCAGGATTGGGCAGAAG | TACGGTAGCAGAGACTTGGTCTCTCTGAGTTCCCTCCTGGACTTG | 194 | 56 | | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__12 | 13 | 32965531 | 32965725 | ACACTGACGACATGGTTCTACACAAGAGCCAGTCCTTGCATACT | TACGGTAGCAGAGACTTGGTCTCTGGAGTGGATGCCATGGTG | 195 | 56 | | Two primers sits in the repeat region |
| BRCA2 | BRCA2_Intron_24__region_3__13 | 13 | 32965663 | 32965858 | ACACTGACGACATGGTTCTACACTGGAGGATCACATGCCTTGG | TACGGTAGCAGAGACTTGGTCTTATTTTGCAGCTTTGTGGTCTGG | 196 | 43 | GAATCGGTGACAGTGGTTTTATAAATTGCTAAGTCCTTTATTGTTTCAGTGACATTTTCTAAAAGGAATTAAAAGCTTTGAAGAATTCTATGCAAGTTCAGAGTAGGCCAGACCACAAAGCTGCAAAATA | One primer sits in the repeat region |
| BRCA2 | BRCA2_113 | 13 | 32968741 | 32968935 | ACACTGACGACATGGTTCTACAAGGCATATTAGAGTTTCCTTTCTTGC | TACGGTAGCAGAGACTTGGTCTTGCAGCAATTAACATATGAGGCTT | 195 | 32 | AGGCATATTAGAGTTTCCTTTCTTGCATCTTAAAATTCATCTAACACATCTATAATAACATTCTTTTCTTTTTTTTCCATTCTAGGACTTGCCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_114 | 13 | 32968830 | 32969028 | ACACTGACGACATGGTTCTACATGCCCCTTTCGTCTATTTGTCAG | TACGGTAGCAGAGACTTGGTCTGCCCTCTTTTGGACTAGCAGAA | 199 | 40 | TGCCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCACTGCAAGCAACCTCCAGTGGCGACCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTTCTGTGTTTTCTGCTAGTCCAAAAGAGGGC | Assays designed by relax mode and have no off-target hits |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| BRCA2 | BRCA2_115 | 13 | 32968930 | 32969107 | ACACTGACGACATGGTTCTACAGCTGCAAGCAACCTCCAGT | TACGGTAGCAGAGACTTGGTCTTACCAAAATGTGTGGTGATGCTG | 178 | 41 | GCTGCAAGCAACCTCCAGTGGCGACCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTTCTGTGTTTTCTGCTAGTCCAAAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAATACTGTTGAGGTAAGGTTACTTTTCAGCATCACCACACATTTTGGTA | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_116 | 13 | 32970934 | 32971113 | ACACTGACGACATGGTTCTACATGGTCCAAACTTTTCATTTCTGCTTT | TACGGTAGCAGAGACTTGGTCTGGGTGGACCACTTGGGA | 180 | 34 | TGGTCCAAACTTTTCATTTCTGCTTTTAAAGGAAATACTTTTGGAAACATAAATATGTGGGTTTGCAATTTATAAAGCAGCTTTTCCACTTATTTTCTTAGAATATTGACATACTTTGCAATGAAGCAGAAAACAAGCTTATGCATATACTGCATGCAAATGATCCCAAGTGGTCCAC | |
| BRCA2 | BRCA2_117 | 13 | 32971050 | 32971232 | ACACTGACGACATGGTTCTACATGCAATGAAGCAGAAAACAAGC | TACGGTAGCAGAGACTTGGTCTTGGCCTCCATATATACTTCTTATAATATTCC | 183 | 40 | TGCAATGAAGCAGAAAACAAGCTTATGCATATACTGCATGCAAATGATCCCAAGTGGTCCACCCCAACTAAAGACTGTACTTCAGGGCCGTACACTGCTCAAATCATTCCTGGTACAGGAAACAAGCTTCTGGTAAGTTAATGTAAACTCAAGGAATATTATAAGAAGTATATATGGAGGCCA | |
| BRCA2 | BRCA2_118 | 13 | 32972189 | 32972375 | ACACTGACGACATGGTTCTACAACTGTGTGTAATATTTGCGTGCTT | TACGGTAGCAGAGACTTGGTCTGTGGAAACAGACTTCCTTTTGGC | 187 | 29 | ACTGTGTGTAATATTTGCGTGCTTAAATATTTTCAATGAAAAGTTACTTTGATTTAGTTTTTTATGTTACTACATAATTATGATAGGCTACGTTTTCATTTTTTTATCAGATGTCTTCTCCTAATTGTGAGATATATTATCAAAGTCCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_119 | 13 | 32972289 | 32972464 | ACACTGACGACATGGTTCTACATTTTTATCAGATGTCTTCTCCTAATTGTG | TACGGTAGCAGAGACTTGGTCTCCAAGGCTCTTCTCTTTTTGCAG | 176 | 39 | TTTTTATCAGATGTCTTCTCCTAATTGTGAGATATATTATCAAAGTCCTTTATCATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTGTCTCAGCCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAGAACTGCAAAAAGAGAAGAGCCTTGG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_120 | 13 | 32972412 | 32972609 | ACACTGACGACATGGTTCTACAAGGGGAGAAAGAGATTGATGACC | TACGGTAGCAGAGACTTGGTCTGGAGAATTCAGTTCTTTTTTCTTTATGGG | 198 | 43 | AGGGGAGAAAGAGATTGATGACCAAAAGAACTGCAAAAAGAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTTTCTCCGGCTGCACAGAAGGCATTTCAGCCACCAAGGAGTTGTGGCACCAAATACGAAACACCCATAAAGAAAAAAGAACTGAATTCTCCTACCTCCACCTGTTAGTCCCATTTGTACATTTGTTTCTCCGGCTGCACAG | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_121 | 13 | 32972486 | 32972684 | ACACTGACGACATGGTTCTACATACCTCCACCTGTTAGTCCCATT | TACGGTAGCAGAGACTTGGTCTGCAAGTTCTTCGTCAGCTATTGA | 199 | 39 | AAGGCATTTCAGCCACCAAGGAGTTGTGGCACCAAATACGAAACACCCATAAAGAAAAAAGAACTGAATTCTCCTCAGATGACTCCATTTAAAAAATTCAATGAAATTTCTCTTTTGGAAAGTAATTCAATAGCTGACGAAGAACTTGC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_122 | 13 | 32972573 | 32972771 | ACACTGACGACATGGTTCTACAACGAAACACCCATAAAGAAAAAGAACT | TACGGTAGCAGAGACTTGGTCTGTGGGAGCAGTCCTAGTGGAT | 199 | 35 | ACGAAACACCCATAAAGAAAAAGAACTGAATTCTCCTCAGATGACTCCATTTAAAAAATTCAATGAAATTTCTCTTTTGGAAAGTAATTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAAACAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCCAC | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_123 | 13 | 32972696 | 32972846 | ACACTGACGACATGGTTCTACACCCAAGCTCTTTTGTCTGGTTC | TACGGTAGCAGAGACTTGGTCTGCCTGGGAACTCTCCTGTTCT | 151 | 44 | CCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAAACAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCCACCAGTTCAGAAGATTATCTCAGACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGC | |
| BRCA2 | BRCA2_124 | 13 | 32972756 | 32972954 | ACACTGACGACATGGTTCTACACTAGGACTGCTCCCACCA | TACGGTAGCAGAGACTTGGTCTACTGGAAAGGTTAAGCGTCAATA | 199 | 40 | CTAGGACTGCTCCCACCAGTTCAGAAGATTATCTCAGACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATTTGCAAAGGCGACAATAAATTATTGACGCTTAACCTTTCCAGT | Assays designed by relax mode and have no off-target hits |
| BRCA2 | BRCA2_3_UTR_1 | 13 | 32972832 | 32972989 | ACACTGACGACATGGTTCTACAGGAGAGTTCCCAGGCCAGTA | TACGGTAGCAGAGACTTGGTCTAATGTGTGGTTTGAAATTATATTCCAGT | 158 | 35 | GGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATTTGCAAAGGCGACAATAAATTATTGACGCTTAACCTTTCCAGTTTATAAGACTGGAATATAATTTCAAACCACCACACATT | |
| BRCA2 | BRCA2_3_UTR_2 | 13 | 32972934 | 32973106 | ACACTGACGACATGGTTCTACATTGACGCTTAACCTTTCCAGTTT | TACGGTAGCAGAGACTTGGTCTTGCAACTGAAGCAAAAGTATACCA | 173 | 35 | TTGACGCTTAACCTTTCCAGTTTATAAGACTGGAATATAATTTCAAACCACACATTAGTACTTATGTTGCACAATGAGAAAAGAAATTAGTTTCAAATTTACCTCAGCGTTTGTGTATCGGGCAAAAATCGTTTTGCCCGATTCCGTATTGGTATACTTTTGCTTCAGTTGCA | |
| BRCA2 | BRCA2_3_UTR_3 | 13 | 32973032 | 32973229 | ACACTGACGACATGGTTCTACATTACCTCAGCGTTTGTGTATCGG | TACGGTAGCAGAGACTTGGTCTCTGGCCTCAAGCACTCCTC | 198 | 42 | TTACCTCAGCGTTTGTGTATCGGGCAAAAATCGTTTTGCCCGATTCCGTATTGGTATACTTTTGCTTCAGTTGCATATCTTAAAACTAAATGTAATTTATTAACTAATCAAGAAAAACATCTTTggctgagctcggtggctcatgcctgtaatcccaacactttgagaagctgaggtgggaggagtgcttgaggccag | One primer sits in the repeat region |
| BRCA2 | BRCA2_3_UTR_5 | 13 | 32973253 | 32973427 | ACACTGACGACATGGTTCTACACATAGGGAGACCCCCATCTT | TACGGTAGCAGAGACTTGGTCTTCTGCATCAAAATAACTGTACTAAGAGA | 175 | 30 | cataggggagaccccatctttacaaagaaaaaaaaaaGGGGAAAAGAAAATCTTTTAAATCTTTGGATTTGATCACTACAAGTATTATTTTACAAGTGAAATAAACATACCATTTTCTTTTAGATTGTGTCATTAAATGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGA | One primer sits in the repeat region |
| BRCA2 | BRCA2_3_UTR_6 | 13 | 32973316 | 32973499 | ACACTGACGACATGGTTCTACATGGATTTGATCACTACAAGTATTATTTTACA | TACGGTAGCAGAGACTTGGTCTAGGAGAACTATTTCATAGTGAGTTACC | 184 | 29 | TGGATTTGATCACTACAAGTATTATTTTACAAGTGAAATAAACATACCATTTTCTTTTAGATTGTGTCATTAAATGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGATAATTCCTTTTAGTTTAGCTACTATTTTAGGGGATTTTTTTTTAGAGGTAACTCACTATGAAATAGTTCTCCT | |
| BRCA2 | BRCA2_3_UTR_7 | 13 | 32973390 | 32973583 | ACACTGACGACATGGTTCTACATGGAATGAGGTCTCTTAGTACAGTT | TACGGTAGCAGAGACTTGGTCTTGCTCAAAAGGAAACACCACTCT | 194 | 34 | TGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGATAATTCCTTTTAGTTTAGCTACTATTTTAGGGGATTTTTTTTTAGAGGTAACTCACTATGAAATAGTTCTCCTTAATGCAAATATGTTGGTTCTGCTATAGTTCCATCCTGTTCAAAAGTCAGGATGAATATGAAGAGTGGTGTTTCCTTTTGAGCA | |
| BRCA2 | BRCA2_3_UTR_8 | 13 | 32973511 | 32973681 | ACACTGACGACATGGTTCTACATGTTGGTTCTGCTATAGTTCCATCC | TACGGTAGCAGAGACTTGGTCTTTTAATTTCAGAGATCACACTGGAATAGT | 171 | 35 | TGTTGGTTCTGCTATAGTTCCATCCTGTTCAAAAGTCAGGATGAATATGAAGAGTGGTGTTTCCTTTTGAGCAATTCTTCATCCTTAAGTCAGCATGATTATAAGAAAAATAGAACCCTCAGTGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAA | |
| BRCA2 | BRCA2_3_UTR_9 | 13 | 32973572 | 32973770 | ACACTGACGACATGGTTCTACATCCTTTTGAGCAATTCTTCATCCTT | TACGGTAGCAGAGACTTGGTCTTGAGTTTGGATGACCATTTTGTTG | 199 | 27 | TCCTTTTGAGCAATTCTTCATCCTTAAGTCAGCATGATTATAAGAAAAATAGAACCCTCAGTGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAATTACTTCAACTAAAAATTCAAATACTTTAAATCAGAAGATTTCAAGTTAATTTATTTTTTTTTTCAACAAAATGGTCATCCAAACTCA | |

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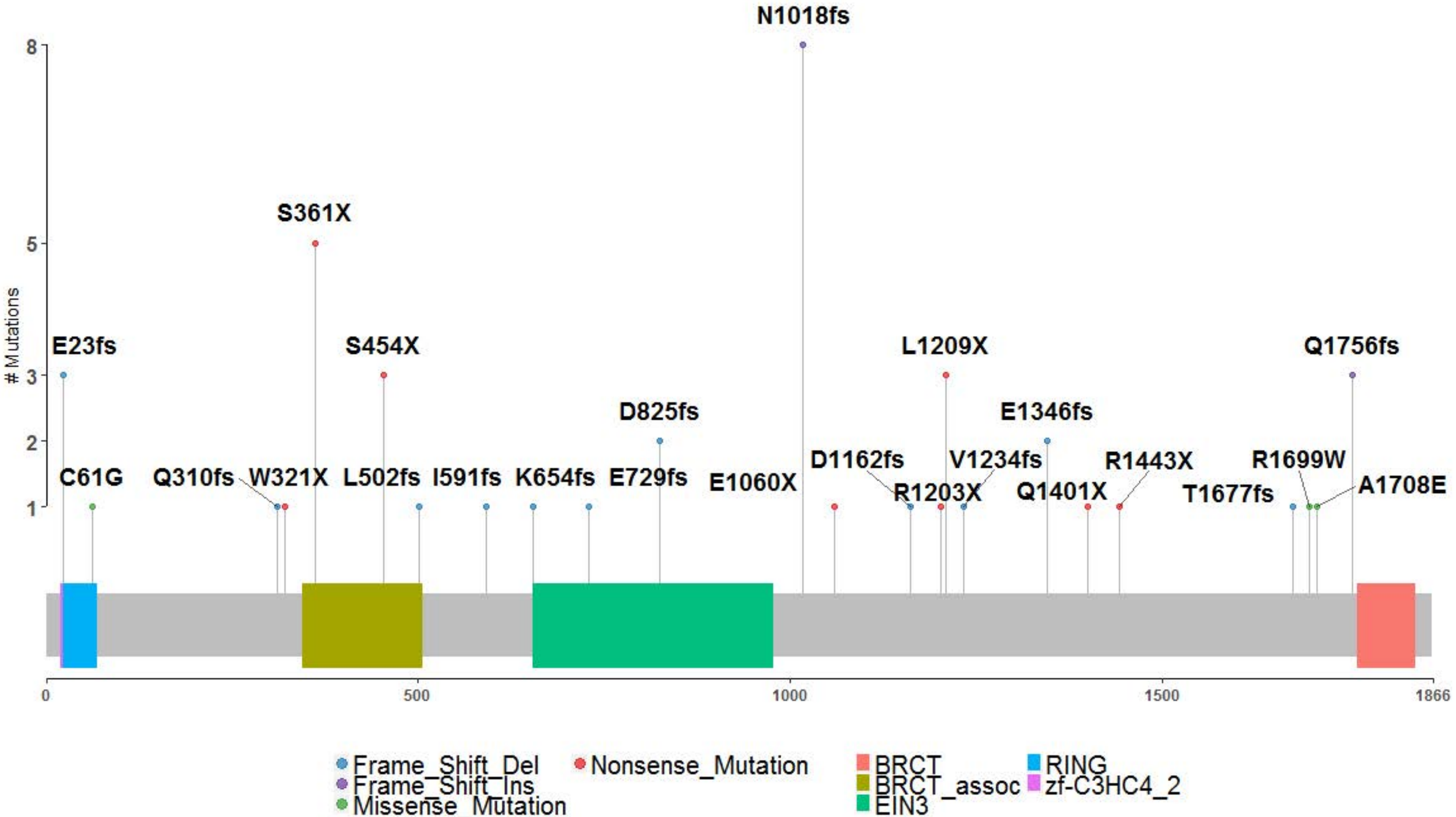
|---|---|---|---|---|---|---|---|---|---|---|
| BRCA2 | BRCA2_3_UTR_10 | 13 | 32973633 | 32973831 | ACACTGACGACATGGTTCTACATGTAACTCTAATTCCTTTTTACTATTCCAGT | TACGGTAGCAGAGACTTGGTCTGCGCTAAAAATAAAGCAGGCAGA | 199 | 28 | TGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAATTACTTCAACTAAAAATTCAAATACTTTAAATCAGAAGATTTCATAGTTAATTTATTTTTTTTTTCAACAAAATGGTCATCCAAACTCAAACTTGAGAAAATATCTTGCTTTCAAATTGGCACTGATTCTGCCTGCTTTATTTTTAGCGC | |
| BRCA2 | BRCA2_3_UTR_11 | 13 | 32973746 | 32973929 | ACACTGACGACATGGTTCTACATCAACAAAATGGTCATCCAAACTCAA | TACGGTAGCAGAGACTTGGTCTaaaaaGGACGTAACAAATGAGAGTAT | 184 | 35 | TCAACAAAATGGTCATCCAAACTCAAACTTGAGAAAATATCTTGCTTTCAAATTGGCACTGATTCTGCCTGCTTTATTTTTAGCGCTATCACAGGACCCAGAGCCTATGCCCTTTTAAACTTACCACAAAAGCAGAAGATTAATTCAATTTAAGATGATACTCTCATTTGTTACGTCCttttt | One primer sits in the repeat region |
| BRCA2_3_UTR | BRCA2_3_UTR_12 | 13 | 32973158 | 32973307 | ACACTGACGACATGGTTCTACACTGAGCTCGGTGGCTCAT | TACGGTAGCAGAGACTTGGTCTAAAGATTTTCTTTTCCCCTTTTT | 150 | 49 | CTGAGCTCGGTGGCTCATGCCTGTAATCCCAACACTTTGAGAAGCTGAGGTGGGAGGAGTGCTTGAGGCCAGGAGTTCAAGACCAGCCTGGGCAACATAGGGAGACCCCCATCTTTACAAAGAAAAAAAAAAGGGGAAAAGAAAATCTTT | |
| BRCA2_Promoter_Combined | BRCA2_Promoter_Combined_14 | 13 | 32888661 | 32888849 | ACACTGACGACATGGTTCTACACTGCGAGGAAGACAGGTGAT | TACGGTAGCAGAGACTTGGTCTGCACGGCTAACTTTGCATTT | 189 | 55 | CTGCGAGGAAGACAGGTGATCCGAATCCTAAGAATGCAAAAGATGGGCCGGGTGTGGTGGCTCATGCCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCACCTGAGGTCGGGAGGTTGAGACCAGACTGACCAACAACGGAGAAACCCCGTCTCTACTTAAAAATGCAAAGTTAGCCGTGC | |
| BRCA2_Promoter_Combined | BRCA2_Promoter_Combined_15 | 13 | 32888792 | 32888990 | ACACTGACGACATGGTTCTACAAGACTGACCAACAACGGAGAA | TACGGTAGCAGAGACTTGGTCTTGAGACGGAGTTTCGCTCTT | 199 | 57 | AGACTGACCAACAACGGAGAAACCCCGTCTCTACTTAAAAATGCAAAGTTAGCCGTGCGTGGTGGCCCATGCCTGTATTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAACCACTTGATCCCTGGAGGCGGAAGTTGCGGTGAGCGGAGATTGCGCCATTGCACACCAGCCCGGGCCACAAGAGCGAAACTCCGTCTCA | |
| BRCA2_Promoter_Combined | BRCA2_Promoter_Combined_16 | 13 | 32888925 | 32889092 | ACACTGACGACATGGTTCTACAGTTGCGGTGAGCGGAGAT | TACGGTAGCAGAGACTTGGTCTCCGTTTCCTTGCTTGAAAAA | 168 | 50 | GTTGCGGTGAGCGGAGATTGCGCCATTGCACACCAGCCCGGGCCACAAGAGCGAAACTCCGTCTCAAAAAAAAAAAGCAAAAGATACTACCAAGCCCTGCGGAGCAAGGTACCTCACACTTCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGG | |

BRCA1 (NM_007294)



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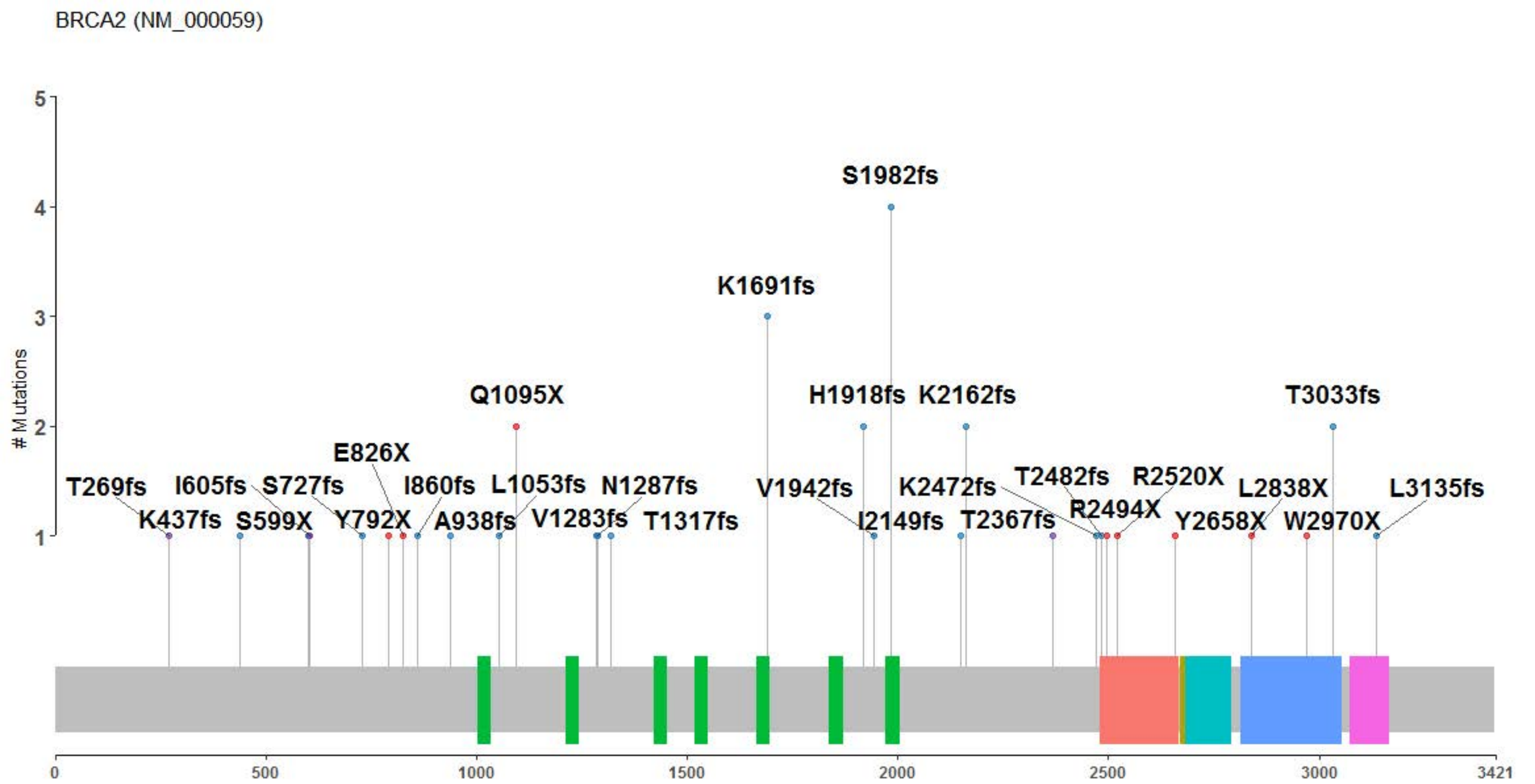

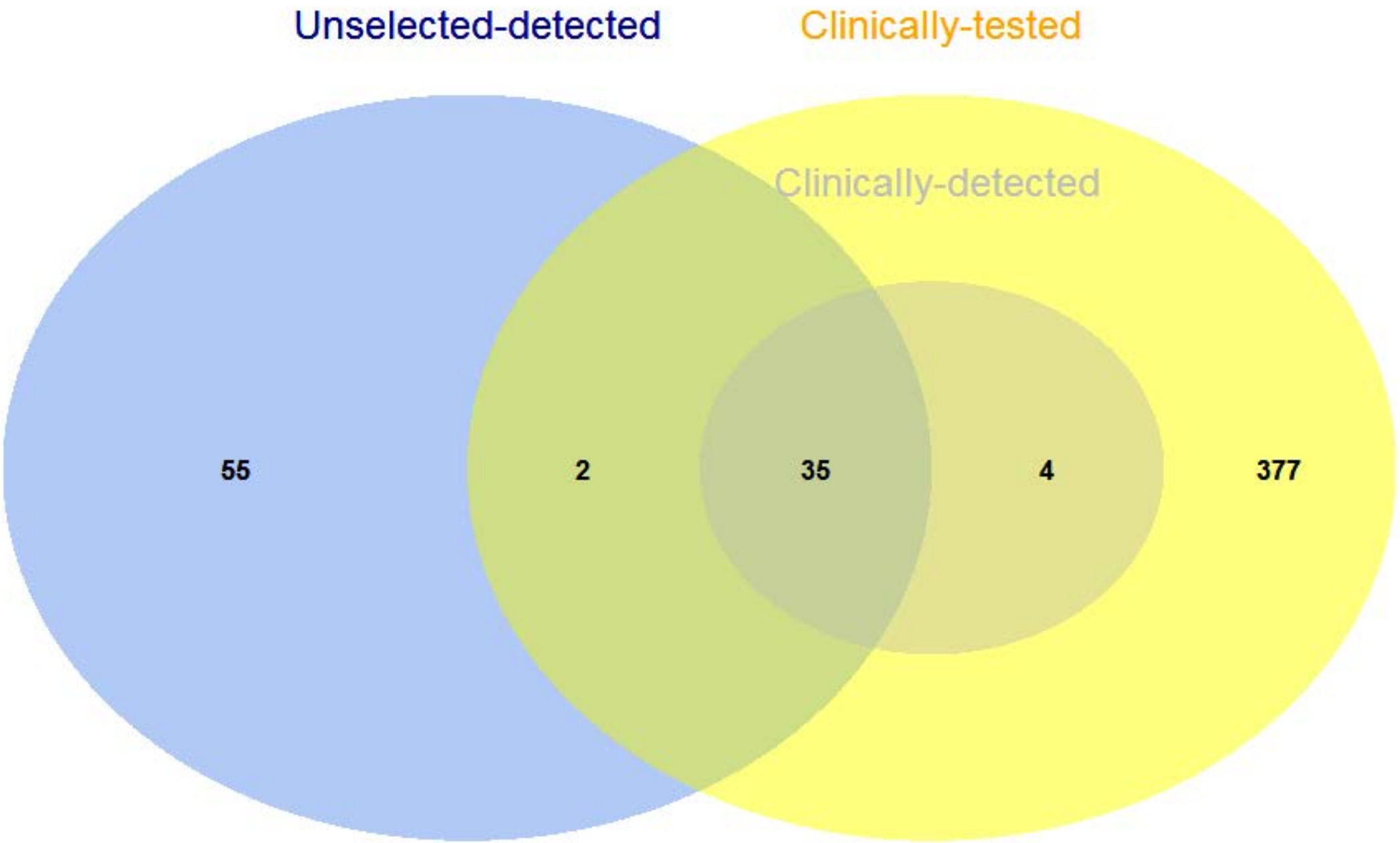
Unselected-detected
Clinically-tested
Clinically-detected
55
2
35
4
377